

# 6 *Managing Your Sequence Projects*

<b>The Main List</b> .....	<b>6-3</b>
What are List Files? .....	6-6
<b>Opening a New or Existing List File</b> .....	<b>6-7</b>
Creating a New List File .....	6-7
Opening an Existing List File .....	6-12
<b>Selecting Sequences</b> .....	<b>6-13</b>
<b>Expanding List Files, RSF Files, and MSF Files in a List</b> .....	<b>6-14</b>
<b>Adding Items to a List</b> .....	<b>6-16</b>
Database Sequences .....	6-16
Single or Multiple Sequence Files .....	6-17
<b>Adding Comments to a List File</b> .....	<b>6-21</b>
<b>List Item Attributes</b> .....	<b>6-22</b>
Viewing Sequence Attributes .....	6-24
Editing List Item Attributes .....	6-25
<b>Deleting Files</b> .....	<b>6-29</b>
Removing Items from a List .....	6-29
Deleting Files from Disk .....	6-29

<b>Searching for Items in a List</b> .....	<b>6-31</b>
<b>Arranging Items in a List</b> .....	<b>6-32</b>
Alphabetically Sorting List Items .....	6-32
Moving a List Item .....	6-32
<b>Reformatting Items in a List</b> .....	<b>6-34</b>
<b>Saving Changes to a List File</b> .....	<b>6-36</b>

The Main List helps you organize your related sequences and output files into project files. For each project you can use the Main List to “build” list files. List files contain a list of sequence specifications, including single database sequences (such as ba:ecoompa), multiple database sequence specifications (such as ba:\*), personal sequence files, MSF files, RSF files, and other list files. To switch from working on one project to working on another, you simply load a different list file into the Main List mode of the Main Window.

From the Main List you can select sequences to submit to programs. In addition, you can define sequence attributes, including sequence ranges, orientation, topology, and weight, as well as concatenations with other sequences.

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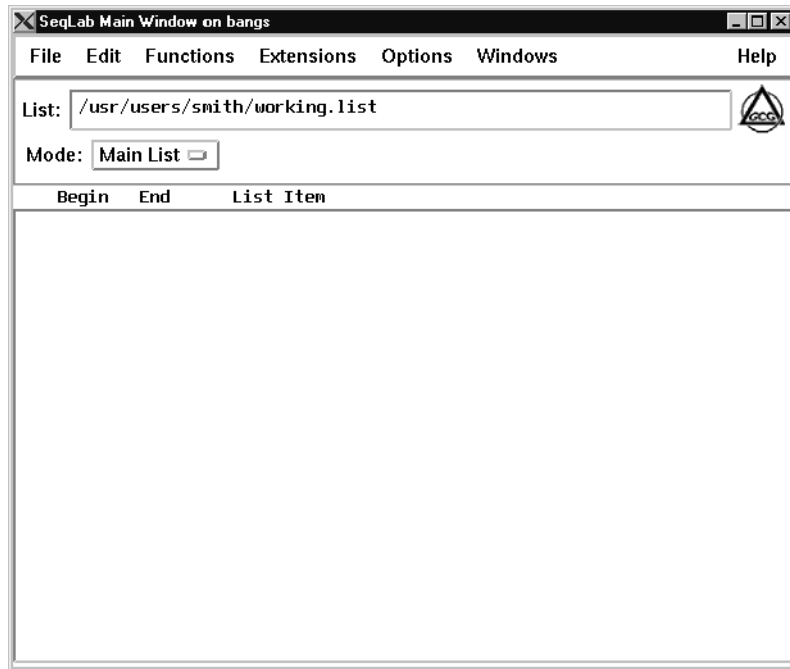
## **The Main List**

The Main List is a project manager that provides a good method of organizing the sequences with which you are working. From this mode, you group project-related sequences and analysis results in list files which you can easily load into the Main List or the Editor. (A list file contains a list of sequences and their locations. For more information about list files, see Appendix C, Types of Sequence Files.)

The Main List lets you point to and use sequences in the databases without first copying them to your directory and thus using up disk space. You can add database sequences, sequences from personal directories, RSF files, MSF files, and nested list files to the Main List. The Main List saves the items you load into a single list file. When you want to switch to a different project, you simply load or create a different list file in the Main List.

The Main List makes it easy for you to work with the sequence files in your projects. From this window you can select sequences to load into the Editor, use sequences as input to a program, add new sequences to or remove sequences from a project, search through items in a list, view and change sequence attributes, and extract sequences into a different format, among other tasks. You can organize these sequences by project and load a different list file into the Main List as needed.

The first time you use SeqLab, the Main List will be empty with the name working.list.



Once you add your sequences to the Main List and create list files, SeqLab opens with the last file you were working with each time you begin a subsequent session with SeqLab.

The illustration below shows the features of the Main List.

Displays the sequence type: nucleic (N), protein (P), ambiguous (\*), or unknown (\*).

Indicates the strand orientation: forward (+) or reverse (-).

Shows the begin and end position of the sequence.

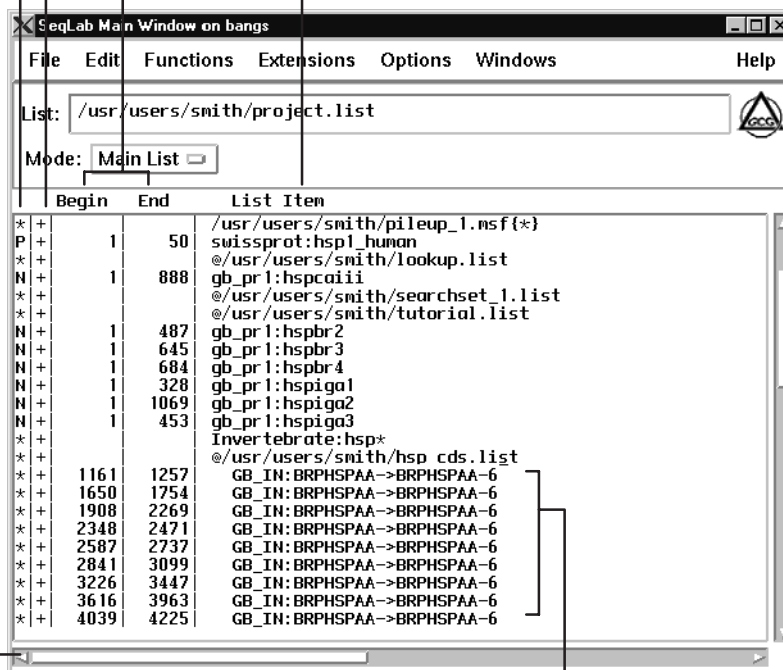
Names each item in the list file currently displayed.

Menu bar

Names the currently loaded list file

Mode selector toggles between Main List and Editor modes.

Scroll bars let you move from left to right, allowing you to view the list item comments on the right.



The → arrow indicates that the sequences can be joined by those programs that support the Join: sequence attribute.

Scroll bars let you display all items in your list—from top to bottom.

**Note:** Some sequences may not display the sequence type, strand orientation, or begin and end positions until you use them as input to a program or until you double-click them to view the sequence attribute information. Because of this, the sequence type may display as ambiguous (\*), the sequence strand orientation may display as a forward strand (+), and the begin and end position may appear blank until you use the sequence.

### ***What are List Files?***

List files are what their name implies: a file containing a list of sequences. You can think of list files as a way to organize your sequences on a project-by-project basis. In addition to database sequences and individual sequences in your own directories, list files also can contain RSF files, MSF files, and other list files. (See Appendix C, Types of Sequence Files.)

List files optionally also may contain sequence attributes, such as the beginning and ending position of the sequence, the strand (forward or reverse), sequence topology (linear or circular), sequence weight, and sequence joining.

For more information about list files and the sequences they can contain, see Appendix C, Types of Sequence Files.

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## Opening a New or Existing List File

Before you can run programs in SeqLab, you must create a new list file or open an existing one. This section teaches you how. For information on how to add sequences to a list file, see “Adding Items to a List” in this chapter.

### Creating a New List File

You can create list files in three ways: 1) the easiest way is to create them from scratch using SeqLab; 2) you can save a subset of sequences from one list file as a new, separate list file; and 3) you can run programs that create list files as their output.

► To create a new list file from scratch:

1. From the Main List, choose New List... from the File menu. The New List File dialog box appears.



2. Click the mouse pointer in the Name of new list file: text box and type the name of the new list file. If you do not specify a directory, the list file will be created in your working directory.
3. Click OK. An empty list window appears with the name of your new list file displayed at the top.

To add sequences to a list file, see “Adding Items to a List” in this chapter.

► To save a subset of sequences from one list file as a separate, new list file:

1. In the Main List, select the sequences you want.
2. From the File menu, choose Save Selected.... The Save Selected List dialog box appears, prompting you to name the new list file.



3. Type the name of the new list file in the Name of Selected List text box and click OK. The list file is written in your working directory, unless you specify a different one.

To open the new list file in the Main List, see “Opening an Existing List File” in this chapter.

► Wisconsin Package programs that produce output in list file format:

Required parameters and the location of the program within the Functions menu also are listed below.

**Note:** *Some of the programs may include additional program-specific information in the output list file. This extra information will not affect the list file's performance.*

Program	Required parameter(s)	Functions menu location
Assemble	In the Assemble program window, select the “List file of output sequence names” toggle button and type a name for the list file in the text box.	Editing and Publication
BLAST	<ol style="list-style-type: none"> <li>1. In the BLAST program window, click Search Set.... The Choose a Search Set for BLAST dialog box appears.</li> <li>2. Choose a local database.</li> </ol>	Database Sequence Searching
Corrupt	In the Corrupt program window, select the “List file of output sequence names” toggle button and type a name for the list file in the text box.	Manipulation
FastA	--	Database Sequence Searching
FastX	--	Database Sequence Searching
FindPatterns	<ol style="list-style-type: none"> <li>1. In the FindPatterns program window, click on Options.... The FindPatterns Options window appears.</li> <li>2. Select the “Format output as a list file of sequence names” toggle button.</li> </ol>	Database Sequence Searching

<b>Program</b>	<b>Required parameter(s)</b>	<b>Functions menu location</b>
FromEMBL	In the FromEMBL program window, select the “List file of output sequence names” toggle button and type a name for the list file in the text box.	Importing/Exporting
FromFastA	In the FromFastA program window, select the “List file of output sequence names” toggle button and type a name for the list file in the text box.	Importing/Exporting
FromGenBank	In the FromGenBank program window, select the “List file of output sequence names” toggle button and type a name for the list file in the text box.	Importing/Exporting
FromIG	In the FromIG program window, select the “List file of output sequence names” toggle button and type a name for the list file in the text box.	Importing/Exporting
FromPIR	In the FromPIR program window, select the “List file of output sequence names” toggle button and type a name for the new list file in the text box.	Importing/Exporting
Motifs	<ol style="list-style-type: none"> <li>1. In the Motifs program window, click Options.... The Motifs Options window appears.</li> <li>2. Select the “Write output file in list file format” toggle button.</li> </ol>	Protein Analysis or Database Sequence Searching
MotifSearch	---	Database Sequence Searching

<b>Program</b>	<b>Required parameter(s)</b>	<b>Functions menu location</b>
Pretty	<ol style="list-style-type: none"> <li>1. In the Pretty program window, select the “Write the individual sequences in a PRETTY file into separate sequence files” toggle button.</li> <li>2. In the “List file of output sequence names” text box, type a name for the list file.</li> </ol>	Multiple Comparison
ProfileSearch	--	Database Sequence Searching
Reformat	In the Reformat program window, select the “List file of output sequence names” toggle button and type a name for the list file in the text box.	Importing/Exporting
Sample	In the Sample program window, select the “List file of output sequence names” toggle button and type a name for the list file in the text box.	Utilities-> Sequence Utilities
SSearch	--	Database Sequence Searching
StringSearch	--	Database Reference Searching
TFastA	--	Database Sequence Searching
TFastX	--	Database Sequence Searching
Translate	In the Translate program window, select the “List file of output sequence names” toggle button and type a name for the list file in the text box.	Translation
WordSearch	--	Database Sequence Searching

## Opening an Existing List File

► To open an existing list file in the Main List:

1. Choose Open List... from the File menu. The Open List File dialog box appears.



2. Use this box to select a list file and click OK. SeqLab loads the selected list file into the Main List.

---

## Selecting Sequences

- ▶ To select one or more sequences from the Main List:

Choose from the following.

- Click or drag the mouse in combination with using <Shift> and <Ctrl> to select sequences. For more information, see “Selecting Items with the Mouse” in the “Using the Mouse” topic of Chapter 1, Basic Concepts.

***Note:** You can select individual sequences within RSF, MSF, and nested list files to analyze or use as input to a program. To do so, expand the RSF file, MSF file, or list file into its individual entries. For more information, see “Expanding List Files, RSF Files, and MSF Files in a List” in this chapter.*

- **Select All.** Choose Select All from the Edit menu to select all sequences currently loaded in the Main List.

---

## **Expanding List Files, RSF Files, and MSF Files in a List**

You can expand nested list files, RSF files, and MSF files to display the individual items within them. Note, however, that you cannot expand a database specification that includes a wildcard, for example `GenEMBL:alu*`. For more information, see Appendix C, Types of Sequence Files.

▶ To expand a nested list file, RSF file, or MSF file in the Main List:

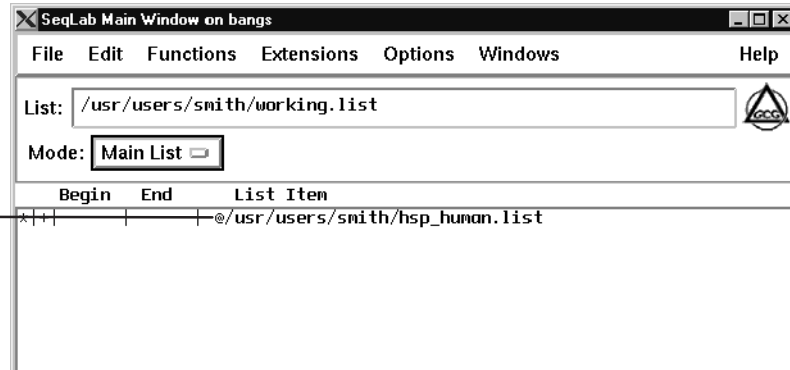
Double-click on the nested list file, RSF file, or MSF file. The entry expands into its individual entries below the item in the Main List. Note that the Main List can display a maximum of 2,000 items. If you expand a file that exceeds that limit, SeqLab displays only enough sequences to reach that limit.

▶ To un-expand an expanded item:

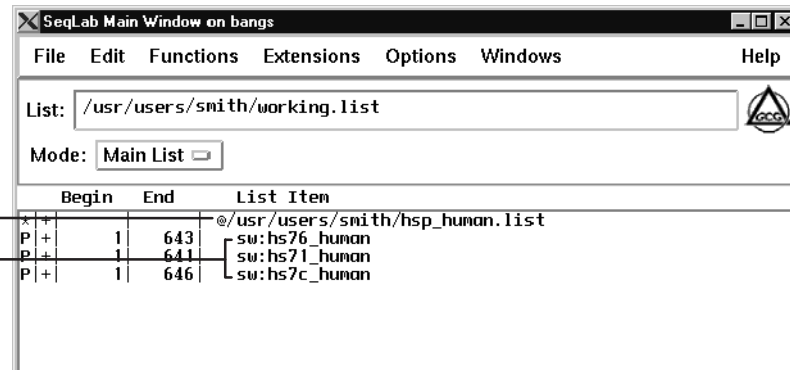
Double-click on the item again to remove the individual entries from the display.

**Note:** *Once you have expanded a list file, RSF file, or MSF file, you cannot use it as input to a program. If you want to select the entire RSF, MSF or list file and it is expanded, double-click on the entry to un-expand it, and then select it.*

List file before expansion



Expanded list file  
Individual entries within an expanded list file. Note that these entries are indented.



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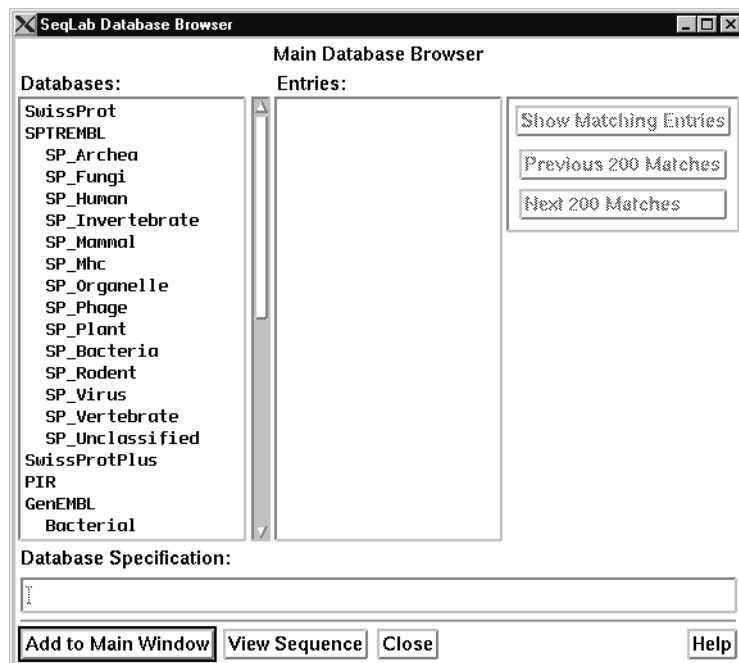
## Adding Items to a List

You can add your own personal sequence files, RSF files, MSF files, other list files, and database sequence files to the Main List.

## Database Sequences

► To add database specifications to the Main List:

From the File menu choose Add Sequences From -> Databases.... The Database Browser appears, allowing you to choose sequences from the various databases available at your site.

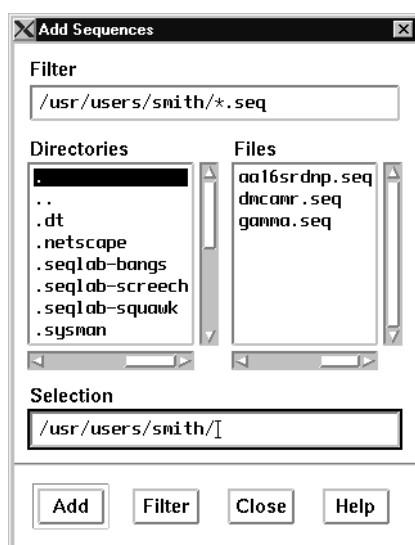


For more information, see Chapter 8, Using the Database Browser.

## Single or Multiple Sequence Files

► To add single sequence files, list files, RSF files, or MSF files to the Main List:

1. From the File menu choose Add Sequences From → Sequence Files.... The Add Sequences file selection box appears, allowing you to choose sequence files from available directories.



2. Select the sequence file(s) you want.

**Note:** You can add only GCG-formatted sequences to the Main List. To add non-GCG-formatted sequences, see the following task.

3. Click the Add button. The sequence(s) are added to the Main List.
4. Click the Close button when you are finished.

► To add non-GCG-formatted sequences to the Main List:

**Note:** You can also add non-GCG-formatted sequences directly into the Editor. To do so, use the *Import...* function from the File menu in the Editor. For more information, see “Loading FastA, GDE, or GenBank Flat Files into the Editor” in the “Loading Sequences into the Editor” section of Chapter 2, *The Editing Sequences and Alignments*.

1. From the Functions menu, click on Importing/Exporting to select from the available programs. Choose from the following:

■ **Reformat.** Formats files created with a text editor to create GCG-format files.

**Note:** The text file you create as input to the Reformat program has specific format requirements. For more information, see *Reformat in the Program Manual*.

■ **FromEMBL.** Reformats files in EMBL flat file format to GCG format.

■ **FromFastA.** Reformats files in FastA format to GCG format.

■ **FromGenBank.** Reformats files in GenBank flat file format to GCG format.

■ **FromPIR.** Reformats files in PIR flat file format to GCG format.

■ **FromIG.** Reformats files in IntelliGenetics format to GCG format.

■ **FromStaden.** Reformats files in Staden format to GCG format.

The main window for the program you selected appears. (For more information on these programs, see the Program Manual.)

2. Choose from the following:
  - If you selected Reformat:
    - a. Click on the “Reformat non-GCG sequence file(s) into GCG format” toggle button.
    - b. Click on the File Specification... button to display and select the file you want to reformat from a file selection box, or type the file specification directly in the text box to the right of the File Specification... button.
  - If you selected FromEMBL, FromFastA, FromGenBank, FromPIR, FromIG, or FromStaden, click on the “*Format* sequence data file...” button to display and select the file you want to reformat from a file selection dialog box, or type the file specification directly in the text box to the right of the “*Format* sequence data file...” button.

**Tip**

If you are reformatting more than one sequence using Reformat, FromEMBL, FromFastA, FromGenBank, FromPIR, FromIG, or FromStaden, the easiest way to recover the output files is to supply a list filename in the “List file of output sequence names” text box. After you run the program, the list file will appear in the Job Manager window, and will contain the names of the individual output files that were created.

3. Select any other optional parameters you want.
4. On the main program window, specify how to run the program by selecting a method from the How: option menu and click Run. The job appears on the Job Manager window, and when it is finished running, output appears on the Output Manager window.

The output is written in your working directory.
5. From the Windows menu, choose Output Manager. The Output Manager window appears.

- 6.** Select the newly formatted GCG sequence file from the list of output files.
  - a.** (optional) If you want to rename the file, click Save As.... A dialog box appears, allowing you to specify a new name. Type the new name and click Save. The dialog box closes and you return to the Output Manager.
  - b.** With the file still selected, click the Add to Main List button.

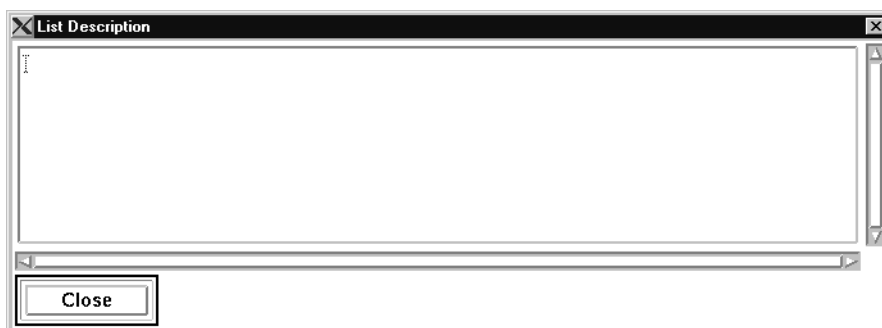
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## Adding Comments to a List File

You can add comments to a list file to help you remember the type of sequences you have included, their significance, and when they were created, among other information.

► To add comments to a list file:

1. In the Main List, open the list file to which you want to add comments.
2. From the Edit menu, choose List Description.... The List Description dialog box appears.



***Note:** If you created a list file as output from a Wisconsin Package program, the program may display program and sequence comments in the List Description dialog box. You can add to or delete from existing comments.*

3. Click the cursor in the window and type your comments.
4. When you are finished, click the Close button. To save your comments, from the File menu, choose Save List.

To view a list file's description, choose List Description... from the Edit menu.

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## List Item Attributes

The items in a list file may have several attributes in addition to their filename or database specification. These attributes include:

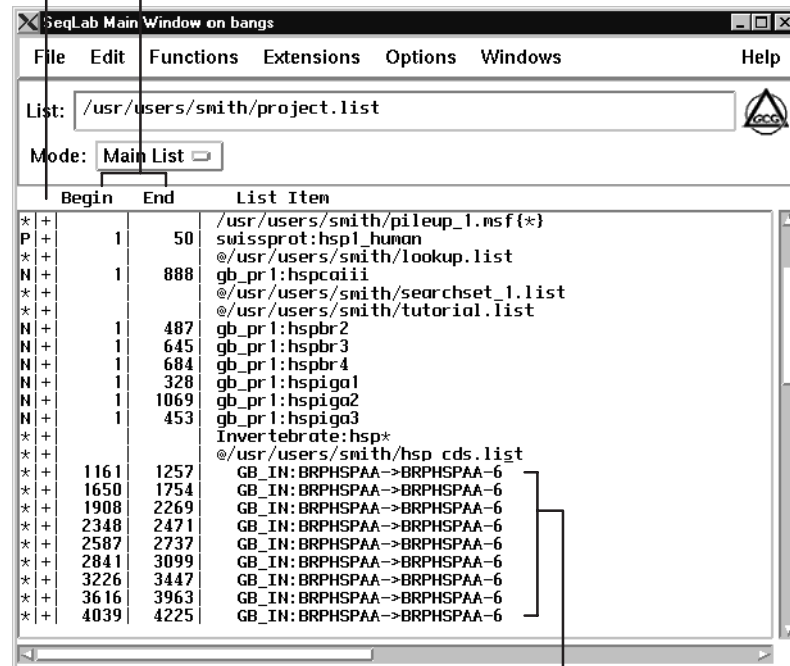
- ◆ **Begin Position.** (Begin:*n*) Shows the base position you want to start with in the sequence, where *n* = 1 to the length of the sequence.
- ◆ **End Position.** (End:*n*) Shows the base position you want to end with in the sequence, where *n* = 1 to the length of the sequence.
- ◆ **Strand: Forward or Reverse.** (Strand:+ or -) Defines the forward or reverse sequence strand, where + = the forward strand and - = the reverse strand.
- ◆ **Sequence Topology: Linear or Circular.** (Circ:F or T) Defines the sequence strand as linear or circular, where F = linear and T = circular.
- ◆ **Sequence Weight.** (Wgt:*n.n*) Defines the significance of the sequence in comparison to other sequences. That is, you may not want all sequences accounted for equally to determine a result. Therefore, you can weight some greater than others. This attribute is of use only when you are using two or more sequences in the analyses.
- ◆ **Join.** Indicates that the sequence is joined, or concatenated, with the next sequence in the list that has an identical "Join: *name*" attribute. (Assemble, Translate, and LookUp are the only Wisconsin Package programs that use the Join attribute.)

**Note:** Currently, *Assemble*, *CodonFrequency*, *Distances*, *Diverge*, *FrameSearch*, *PileUp*, *PlotSimilarity*, *ProfileMake*, *Seg*, *Translate*, and *Xnu* use some or all of these sequence attributes.

The Main List window displays some of the sequence attributes. To view all sequence attributes, see “Viewing Sequence Attributes” next in this chapter.

**Strand:**  
forward (+) or reverse (-).

**Begin position and  
End position**

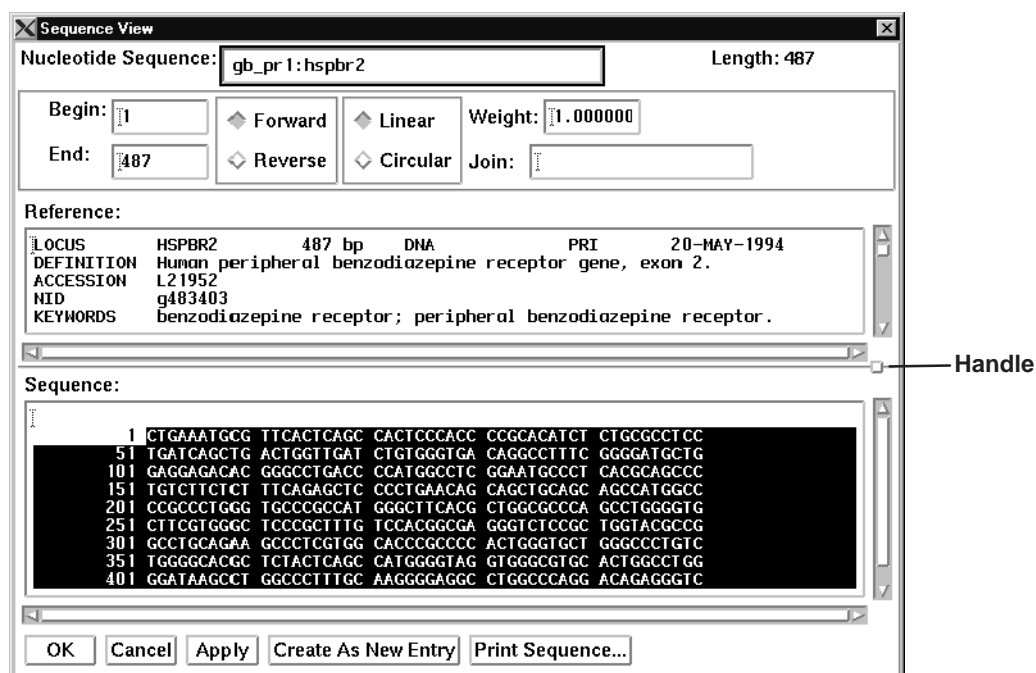


**Join:**  
Sequences with identical join names can be concatenated into a single sequence. The join name appears to the right of the → arrow.


## Viewing Sequence Attributes

- ▶ To view the attributes of items in a list:

In the Main List, double-click on the single sequence you want to view. A Sequence View dialog box appears, displaying the sequence attributes as well as the reference and sequence itself.



You can view the attributes of only single sequences by double-clicking on them. You cannot view multiple sequence specifications in this manner.

 **Tip** Click and hold on the handle and drag vertically to resize the Reference: or Sequence: paned windows.

## Editing List Item Attributes

You can modify the attributes of a single sequence at a time, multiple sequences in a list, or the entire list.

► To change the attributes of a single sequence:

**Note:** You cannot edit an item that is within a nested list, RSF, or MSF file. If you try to do so, SeqLab asks whether you want to copy that edited item to the Main List as a separate sequence.

1. Double-click on the sequence you want to modify. An expanded Sequence View dialog box appears.

You can edit the attributes area only.

Sequence View

Nucleotide Sequence:  Length: 487

Begin:   Forward  Linear Weight:

End:   Reverse  Circular Join:

Reference:

LOCUS	HSPBR2	487 bp	DNA	PRI	20-MAY-1994
DEFINITION	Human peripheral benzodiazepine receptor gene, exon 2.				
ACCESSION	L21952				
NID	g483403				
KEYWORDS	benzodiazepine receptor; peripheral benzodiazepine receptor.				

Sequence:

```


1 CTGAAATGCG TTCACTCAGC CACTCCCACC CCGCACATCT CTGGCCTCC
51 TGATCAGCTG ACTGGTTGAT CTGTGGGTGA CAGGCCTTTC GGGGATGCTG
101 GAGGAGACAC GGGCCTGACC CCATGGCCTC GGAATGCCCT CACGCAGCCC
151 TGTCITCTCT TTCACAGCTC CCCTGAACAG CAGCTGCAGC AGCCATGGCC
201 CCGCCCTGGG TGCCCGCCAT GGGCTTCAGC CTGGCCCCA GCCTGGGGTG
251 CTTCTGGGC TCCCGCTTTG TCCACGGCGA GGGTCTCCG TGGTACGCCG
301 GCCTGCAGAA GCCCTCGTGG CACCCGCCCC ACTGGGTGCT GGGCCCTGTC
351 TGGGGCACGC TCTACTCAGC CATGGGTAG GTGGCGTGC ACTGGCCTGG
401 GGATAAGCCT GGCCCTTTC AAGGGAGGC CTGGCCAGG ACAGAGGGTC
  
```

OK Cancel Apply Create As New Entry Print Sequence...

**Note:** The reference and sequence areas are displayed only when you double-click on a single sequence. If you choose Change Attributes from the Sequences menu, only the attribute and action button areas are available.

The reference and sequence areas are display only (non-editable), and you can use the scroll bars to view information that is out-of-view. If the item is a database sequence, the reference area contains information such as the sequence name, definition, accession number, keywords, source, begin and end positions of known sequence features, and known other information.

---

 **Tip** To change the begin and end positions of a sequence, type directly in the Begin: and End: text boxes. Or, click and drag to highlight the area of interest in the Sequence: area of the dialog box and click the Apply button. The Begin: and End: text boxes change to reflect the portion of the sequence you highlighted.


---

2. Change the attributes you want by typing in the text boxes or clicking the appropriate radio buttons in the attributes area.

*Note:* To edit the sequence characters, load the sequence into the Editor.

3. Save your changes and return to the Main List. Choose from the following action buttons:
  - **OK.** Changes the attributes for the selected entry in the Main List to the values currently specified in the Sequence View dialog box, and the dialog box closes.
  - **Cancel.** Closes the dialog box without applying any changes since the last Apply to the selected entry in the Main List.
  - **Apply.** Changes the attributes for the selected sequence in the Main List to the values currently specified in the Sequence View dialog box. The dialog box remains open.
  - **Create As New Entry.** Adds a new entry to the top of the Main List, using the sequence attributes currently specified in the Sequence View dialog box. The dialog box remains open.

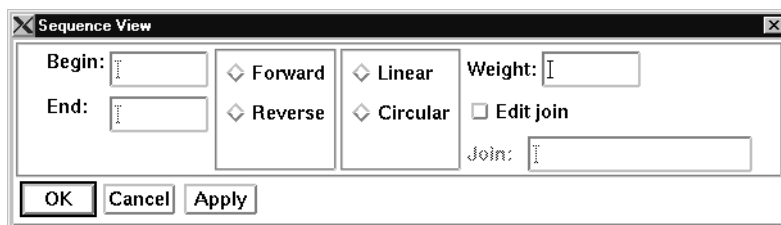
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 **Tip** Use the Create As New Entry button to create items in the Main List that are duplicates of existing sequences *except* for their attribute values. That is, you could have multiple copies of a sequence in a list file, each copy varying the sequence attributes. This option may come in handy if you find yourself changing the attributes of existing sequences temporarily to use with select programs.

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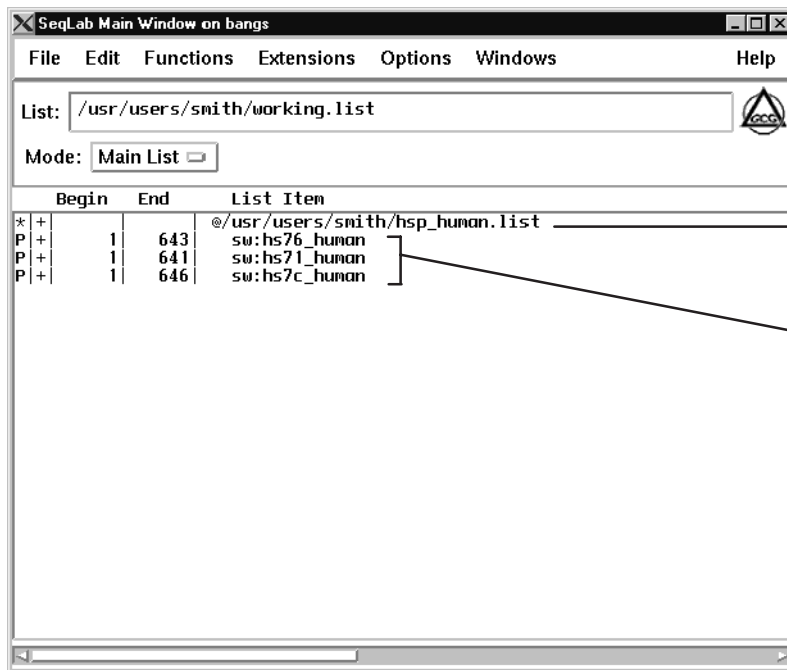
- **Print Sequence....** Displays a Print Text dialog box, from which you can specify a printer. The sequence data, excluding the attributes, is printed. For more information, see “Printing from the Main List or from the Database Browser” in Chapter 12, Printing.

- To change the attributes of multiple sequences in a list or an entire list:
1. Select the sequences of interest from the Main List. You can select single sequence entries, database entries, MSF files, RSF files, or nested list files. To change attributes for all sequences, choose Select All from the Edit menu.
  2. Choose Sequence Attributes... from the Edit menu. The Sequence View dialog box appears.



3. Edit the attributes you want. To change the Join: attribute, click the Edit join toggle button, then add or modify the join name in the Join: text box.
4. Click Apply to save the attribute changes.
5. Click OK to exit from the dialog box.

If you change the attributes of an RSF, MSF, or nested list file, those attributes take precedence over any attributes specified for individual sequences within those files. Note that the attributes you specify for an RSF, MSF, or nested list file appear next to the item on the Main List. However, if you double-click on the file to expand it into its contents, the individual sequences within those files maintain their original attributes. This is advantageous if the individual sequence attributes are of scientific value.



You can change the attributes for an entire list, RSF, or MSF file.

The individual items within the file maintain their attributes.

---

## **Deleting Files**

At some point you probably will want to clean up your list files and delete items within them that are no longer of interest to you. You can do this by loading a list into the Main List and selecting those items you do not want.

You have two options for deleting items: 1) you can simply remove the item(s) from the list, but the file remains in its current directory in case you want to use it later, or 2) you can delete the file from disk.

Note that you cannot remove individual items from within an RSF, MSF, or nested list file that is expanded into its individual items. If you choose an item from within an RSF, MSF, or nested list file and try to remove it, you will get an error message. To remove an item from a nested list file, you must open that file separately in the Main List and delete the item. To remove sequences from an RSF or MSF file, load the file into the Editor and modify it as necessary.

### **Removing Items from a List**

► To remove items from a list:


1. Select the sequences you do not want.
2. From the Edit menu choose Remove from List. The selected sequences are removed from the Main List.

### **Deleting Files from Disk**

► To delete files from disk:

1. Select one or more items from the Main List that you do not want.
2. From the Edit menu choose Delete File from Disk.... SeqLab prompts you before deleting the file(s) from disk.

---


 **Tip** One way to remove one or more sequences in an MSF file is to “comment out” those you do not want. If you comment out sequences instead of deleting them, you can uncomment them and use them at a later time.

To comment out sequences, follow these steps:

1. From the operating system prompt, open the MSF file in the text editor of your choice, for example (OpenVMS) EDT or EVE or (UNIX) vi.
2. Find the sequences you do not want to use in the Name/Weight area toward the top of the file.
3. Type an exclamation point (!) in front of the “Name:” of each sequence you do not want. Consider the illustration below:

```
Picornavirus capsid proteins

Picornavirus.Msf MSF:100 Type: P September 1, 1994 01:53 Check:541 ..
!Name: Cb3          Len: 100          Check: 7009          Weight: 1.00
!Name: E            Len: 100          Check: 60             Weight: 1.00
Name: Plm           Len: 100          Check: 7401          Weight: 1.00
Name: Pls           Len: 100          Check: 6071          Weight: 1.00
```

**Comment out unwanted sequences with an exclamation point (!).** 

4. Save the file and exit the text editor. Only those file that are not commented out will appear when you expand the MSF file in the Main List.
-

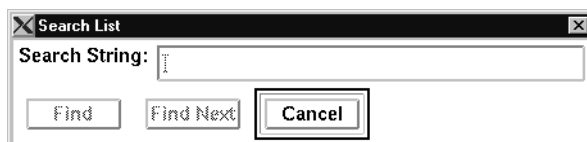
---

## Searching for Items in a List

Sometimes list files may become very large, and you may find it difficult to identify a particular item you are looking for. In such a case, SeqLab has a Find... function that lets you search the sequence and comments area for a particular word or string of words. SeqLab searches only through the list item names and comments that appear in the Main List—it does not search through sequence reference information or through sequence data. In addition, SeqLab does not search through RSF, MSF, or nested list files *unless* you first expand them (see “Expanding List Files or MSF Files in a List” in this chapter). Also, SeqLab does not search through the sequences implied by multiple sequence specifications using a wildcard (\*).

► To search for items in the Main List:

1. From the Edit menu, choose Find.... The Search List dialog box appears, with a text area to enter the text string you want to search for.



2. Enter the text you want to search for and click the Find button. SeqLab searches for the first occurrence of the string in all the sequences that currently appear in the Main List. If a match is found, it is selected and scrolled to the top of the Main List.
3. Click the Find Next button to find the next occurrence of the string, or click Cancel to end the search.

---

## Arranging Items in a List

The Main List displays sequences in the order you added them to the list. However, you may find it useful to organize your sequences alphabetically. Or, you might want to arrange sequences so that those you use most often appear at the top of the list.

### Alphabetically Sorting List Items

► To sort the items in the Main List into alphabetical order:

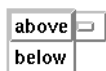
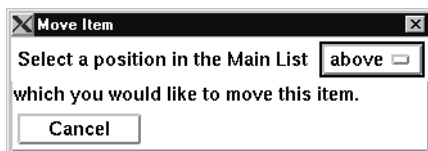
Choose Sort from the Edit menu. SeqLab sorts the sequences alphabetically. To save the changes for next time you log in, choose Save List from the File menu.

### Moving a List Item

**Note:** You cannot move an item that is part of an expanded list (that is, an item within a nested list, RSF, or MSF file). You also cannot select an item within an expanded list, RSF, or MSF file as the location where you'd like to move a chosen item.

► To move sequences from one position in a list to another:

1. Select the sequence(s) you want to move.
2. Choose Move... from the Edit menu. The Move Item dialog box appears, instructing you to select the location in the Main List where you want to move the item.



3. Click on the option menu to choose whether to move the item above or below your chosen location. If you want to change this option, do so before selecting your location. Or, to cancel the move, click the Cancel button.

4. Click above or below the sequence in the Main List where you want to insert the moved sequence. The sequence is moved and the dialog box closes.
5. (optional) To save the changes for the next time you log in, choose Save List from the File menu.

---

## Reformatting Items in a List

You can reformat items in a list file into GCG, Staden, IntelliGenetics, PIR, or FastA format. You can do this in two ways: 1) use the Extract Sequence... function from the Edit menu on the Main List, or 2) use the programs Reformat, ToStaden, ToIG, ToPIR, or ToFastA from Importing/Exporting in the Functions menu. Note that sequences you reformat into Staden, IntelliGenetics, or PIR format cannot be used by SeqLab.

- ▶ To reformat a sequence into GCG, Staden, IntelliGenetics (IG), PIR, or FastA format:

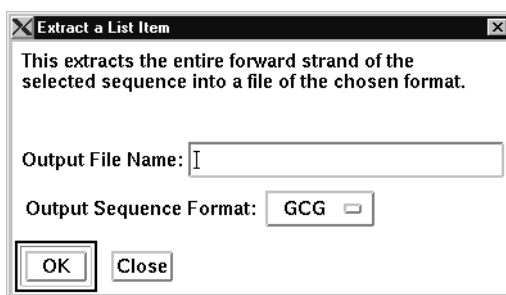
Choose from the following.

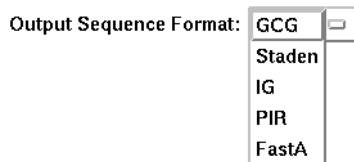
### ■ Use the Extract Sequence... function.

1. Select one item from the Main List. That item can be a single sequence specification or a multiple sequence specification, such as a list, RSF, or MSF file.

***Note:** You can format only single sequence specifications into Staden format.*

2. Choose Extract Sequence... from the File menu. The Extract a List Item dialog box appears.





3. (optional) Click the cursor in the Output File Name: text box and change the name you want the output file saved as.
4. Click the Output Sequence Format: option menu to display the format types and choose one.
5. Click the OK button. The output file is written into your working directory, or the directory you specified in the Output File Name: text box.

**Note:** *If you choose IG or PIR format, only one output file is created, even if the item contains multiple sequence specifications.*

*If you choose GCG format, and the selected sequence is a multiple sequence specification, then multiple files are written into your working directory, and the Output File Name: specification is ignored. (SeqLab uses the sequence name for the filename and the database name in the extension, for example `ldbh_chick.swissprot`.) You may want to use the Reformat program, which allows you to create an output list file in addition to the newly reformatted sequence files.*

- **Use one of the Importing/Exporting programs: Reformat, ToStaden, ToIG, ToPIR, or ToFastA.** For more information, see the Program Manual.

---

## Saving Changes to a List File

The changes you make to a list file while it is open in the Main List are not saved unless you explicitly save them.

► To save changes you have made to a list file:

Choose one of the following from the File menu.

- **Save List.** Saves the changes into a list file of the same name.
- **Save List As....** Saves the changes into a list file of a different name.



- **Save Selected....** Saves only the selected (highlighted) sequences into a list file with a name you specify.



**Note:** If you do not specify a directory, SeqLab saves the file in your working directory.