



**User's Manual
for
PatentIn Version 3.0**

22 June 2000

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SECTION 1
INTRODUCTION

SECTION 1 INTRODUCTION

1.1 PURPOSE

PatentIn 3.0 facilitates the creation of patent applications for genetic sequences. It accepts data about the patent application, validates the data, and creates a sequence listing file for submission. This manual describes how to use PatentIn 3.0.

1.2 CONVENTIONS

Consistent visual cues and standard keyboard operations are used throughout this manual. These conventions are listed in Table 1-1 below.

Table 1-1: Document Conventions

Notation	Represents	Example
	Process the command with a mouse action.	 Select Open from the file menu.
	Process the command with the keyboard.	 Enter changes into the Edit field.
Bold type	Name of a function, file, menu item, or programming construct.	 Click on Exit .
	An informative message to the user.	 NOTE: These fields are mandatory.

1.3 OVERVIEW

PatentIn 3.0 is a computer program designed to expedite the preparation of United States Patent and Trademark Office (USPTO) patent applications containing nucleic acid and polypeptide sequences.

PatentIn 3.0 complies with all format requirements specified in WIPO ST.25 and the related U.S. final rule, "Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Disclosures." It runs on Windows 95, Windows 98, and on Windows NT. Screen displays in Spanish, French, and German will become available in a later release.

For ease of use, the design follows standard Windows user interface conventions.

PatentIn 3.0 includes the following tools:

- **A Sequence Editor**

The primary tool within PatentIn 3.0 is the sequence editor, which enables you to enter and modify both nucleic acid and protein sequence listings, as well as import sequence

listing files created by another editor or word processor (provided they are stored as ASCII text files).

When working in PatentIn 3.0 you may enter data in any order, and also add, remove, or revise **sequence listing** data at any time. You may also save a partially completed application and finish it at a later time.

- **A Sequence Generator**

After you have entered all the data necessary for your patent application, PatentIn 3.0 enables you to generate your application. The application consists of a computer-readable file containing a sequence listing file, which is prepared in accordance with the WIPO ST.25 standard.

SECTION 2
SYSTEM REQUIREMENTS AND PATENTIN 3.0 ACCESS

SECTION 2

SYSTEM REQUIREMENTS AND PATENTIN 3.0 ACCESS

2.1 SYSTEM REQUIREMENTS

PatentIn 3.0 is a self-contained application that can be downloaded from the United States Patent and Trademark Office (USPTO) web site. It operates in a Windows 95/98/NT environment. A minimum of 64 MB of memory is recommended. Additional memory may be required for large patent applications. Very large projects, projects with 100,000 sequences or a sequences approaching 1M, will need a minimum of 128 MB of memory. The disk space required to install PatentIn 3.0 is 2 MB. Additional disk space is required to store project files and sequence listing files.

For PatentIn to work correctly, the "TMP" environment variable must point to a valid directory, and the "PATH" environment variable must include the DOS backup command in the path. Most Windows installations will meet these requirements.

i Special Note for users with very large sequences and large numbers of sequences:PTO has located a viewers that really works for very large text files. A 60 day evaluation version is downloadable at www.fileviewer.com <<http://www.fileviewer.com>> . The viewer is named "V" and version 2000 SR-1. It was tested with 60MB and 120MB files and "worked great." It should manage files of just about any size. It was tested on a laptop with Win98. (LocalAdmin may be required for installation)

2.2 PATENTIN 3.0 ACCESS

PatentIn 3.0 can be downloaded onto your personal computer. The program can be downloaded from the USPTO web page. The Universal Resource Locator (URL) from which the PatentIn 3.0 application can be obtained is: <http://www.uspto.gov/web/offices/pac/patin/patentin.htm>. Follow the instructions found on the Web page to download PatentIn 3.0 and install it on your PC. Upon completing the installation, an icon will be placed on your desktop. Access to the PatentIn 3.0 application program occurs when you double click on the PatentIn 3.0 icon.

SECTION 3
GETTING STARTED

SECTION 3 GETTING STARTED

3.1 PATENTIN 3.0 SEQUENCE

When you first access PatentIn 3.0 by double clicking on the PatentIn 3.0 icon on your desktop, you have immediate access to the PatentIn 3.0 Sequence Screen.

The PatentIn 3.0 Sequence Screen (Figure 3-1) is the main screen.

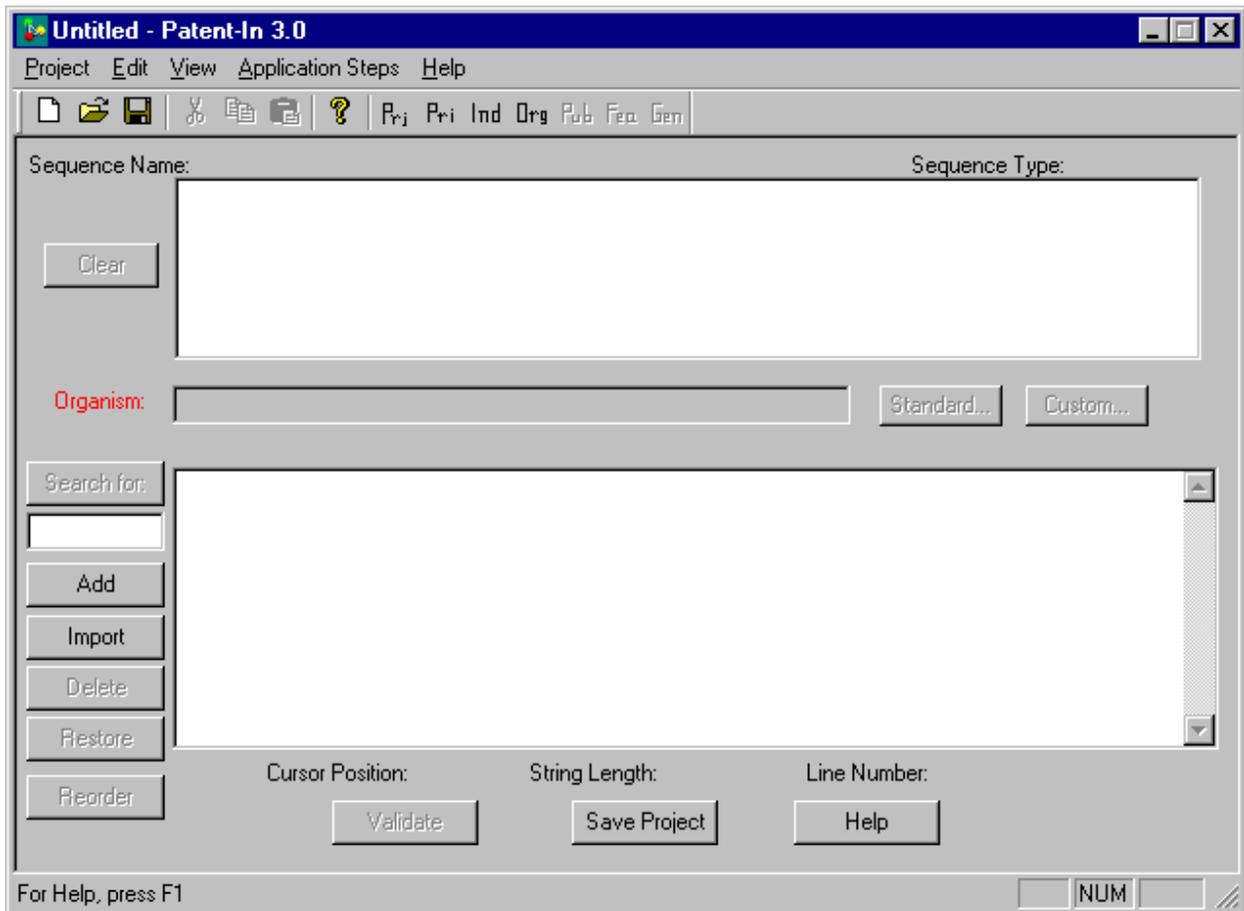


Figure 3-1: PatentIn 3.0 Sequence Screen

The PatentIn 3.0 Sequence Screen (Figure 3-1) provides the user with five drop down menus. Three of which provide access to the real-time system interface. They are Project, Application Steps, and Help. The remaining two drop down menus, Edit and View, are general Microsoft® Windows type menus. The user may select any one of the three drop-down menus when a project is begun. PatentIn 3.0 presents an empty project upon startup. The user can open an existing project with the PatentIn 3.0 Project Menu (Figure 3-2).

3.2 PATENTIN 3.0 PROJECT MENU

The PatentIn 3.0 Project Menu (Figure 3-2) enables you to create and save a project. Selecting “Save” displays the Save As (Figure 3-3) where a new project is given a name and is saved. Selecting “Open” displays the Open Screen (Figure 3-4) where the user can select a previously saved project to open. The “Exit PatentIn 3.0” selection closes the application. Menu items that require a project to be opened, or an output file to be present, are grayed out until those conditions are met.

The PatentIn 3.0 Project Menu (Figure 3-2) selections are shown below. The user will see a list of selectable Menu Items under the Project menu and the active project name on the upper left-hand corner of the screen. In this case Untitled is shown as no project has yet been opened or saved.

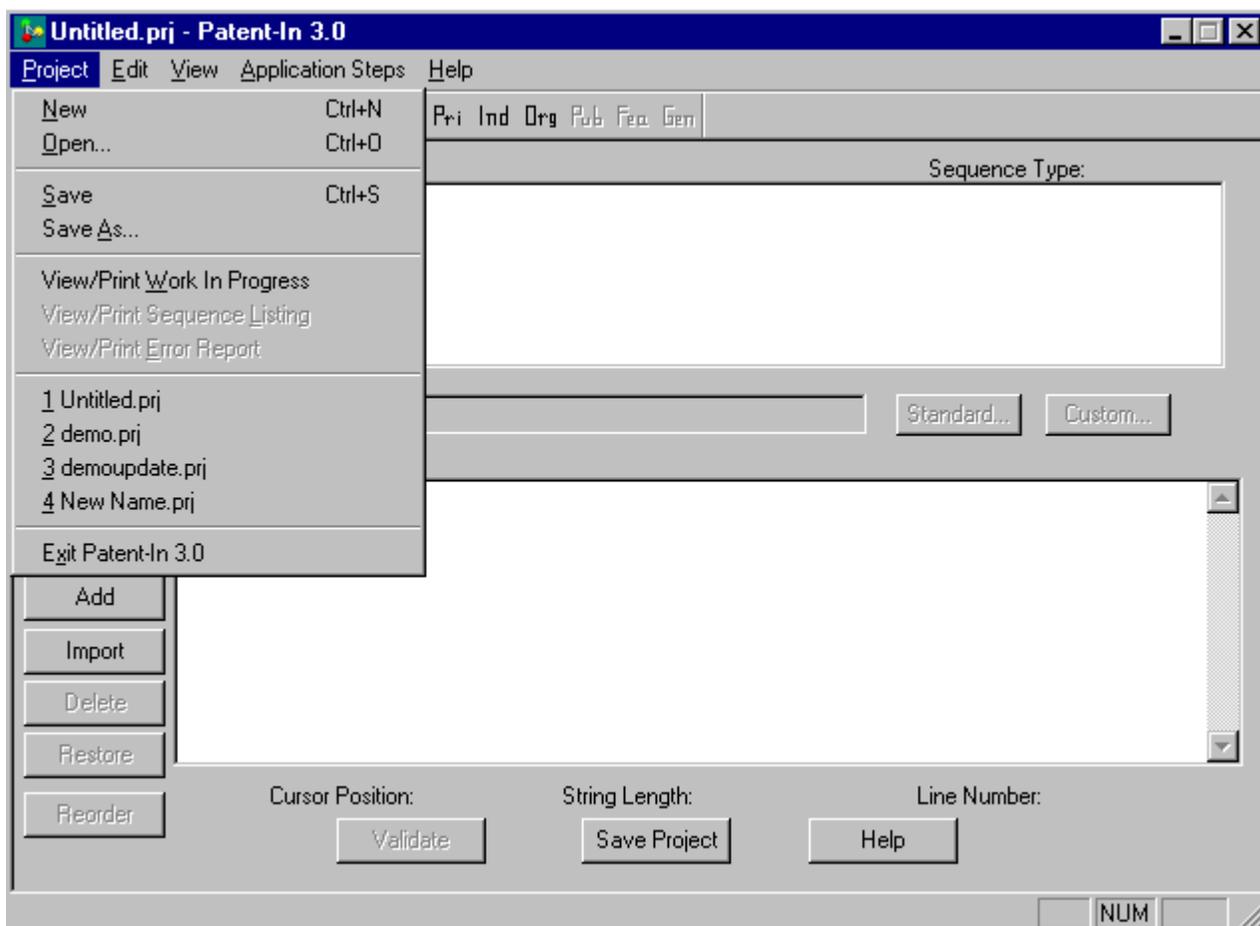


Figure 3-2: PatentIn 3.0 Project Menu

3.3 CREATING AND SAVING A NEW PROJECT

To create and save a new project:

Begin building the new file upon opening the main screen, PatentIn 3.0 Sequence Screen, or:

1.  Select **New** from the Project menu. This clears the all of the current project information.
2.  Select Save from the Project menu. The Save As Screen (Figure 3-3) appears.
3.  Enter the new file name into the **File Name** dialog box.
4.  Click on **Save** to create the new file.
5. The name for the new project will be displayed on the upper left-hand corner of the screen.

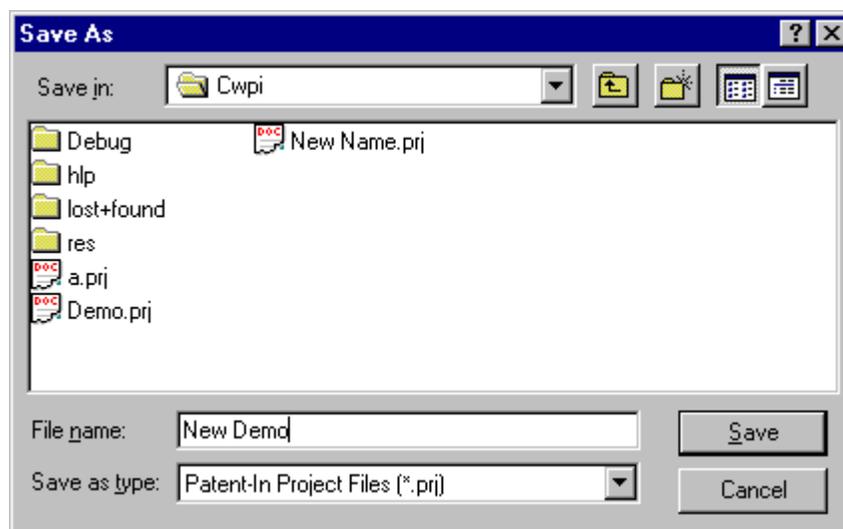


Figure 3-3: Save As Screen

3.4 OPENING A PROJECT

To open an existing project:

1. Select **Open** from the **Project** menu. The Open Screen (Figure 3-4) appears.
2. Open the directory where the file is located.
3. Double-click on the file name to open the file.
4. You are returned to the main screen. The name of the opened project is displayed in the upper left-hand corner of the screen, indicating the project is active.

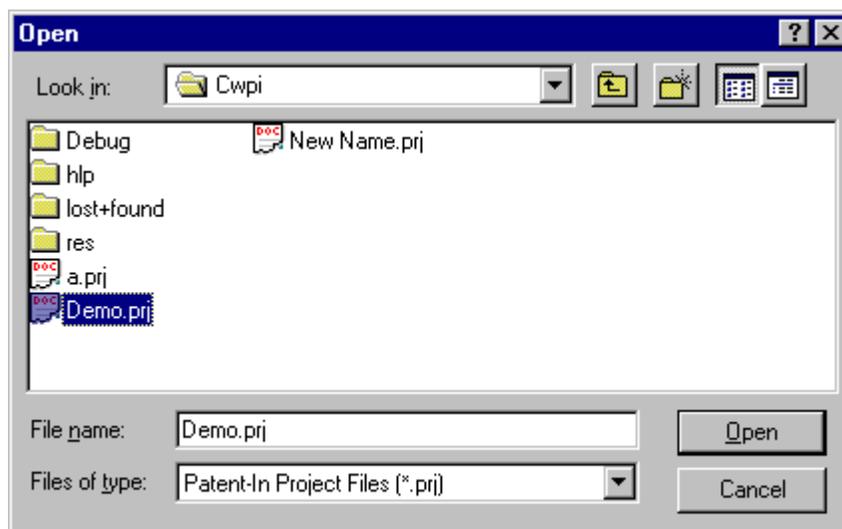


Figure 3-4: Open Screen

i SPECIAL NOTE FOR USERS WITH VERY LARGE SEQUENCES AND LARGE NUMBERS OF SEQUENCES: it takes some time for a large project to clear from memory. This is especially noticed when immediately reopening the project.

3.5 SAVING A PROJECT

To save a Project:

When a project is saved for the first time, the user is automatically prompted to enter a file name.

1.  Select **Save** from the **Project** menu. The Save As Screen (Figure 3-5) will appear if the project has not previously been named. Otherwise, the project will be saved as the previously opened or created name.
2.  Select the directory where you want to save the file.
3.  Type the new file name in the **File Name** dialog box.
4.  Click on the **Save** button to save the project with the new file name.
5. PatentIn 3.0 returns you to the main screen. The new name is displayed in the upper left-hand corner of the screen, indicating that the project is active.

To save under a different file name:

1.  Select **Save As** from the **Project** menu. The Save As Screen (Figure 3-5) will appear.
2.  Select the directory where you want to save the file.
3.  Type the new file name in the **File Name** dialog box.
4.  Click on the **Save** button to save the project with the new file name.
5. PatentIn 3.0 returns you to the main screen. The new name is displayed in the upper left-hand corner of the screen, indicating that the project is active.

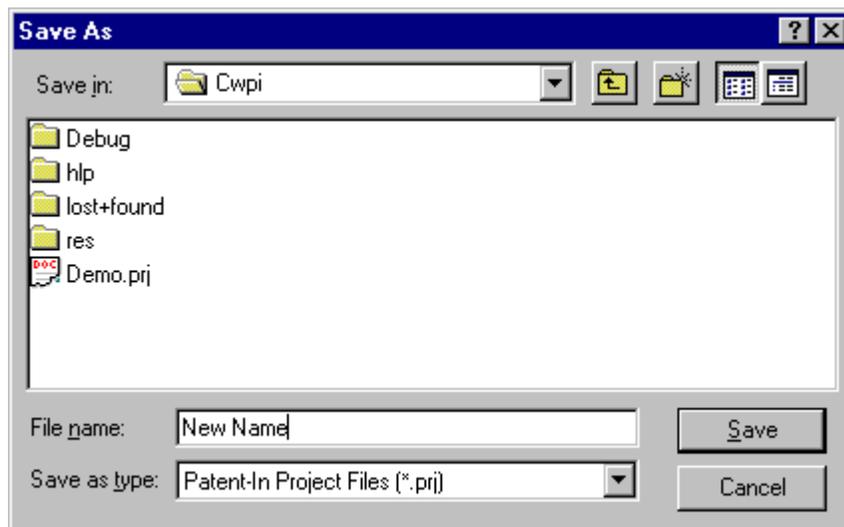


Figure 3-5: Save As Screen

3.6 VIEWING A WORK FILE

The user can view the current work in progress by creating a work file. This work file provides a vehicle for the user to view the data for the entire project in a single place instead of reviewing each individual screen.

To see the Work File:

From the Project Menu,  select **View/Print Work in Progress**.

 Note: This work file was built by selecting **Create Work File**.

3.7 VIEWING WORK IN PROGRESS

PatentIn 3.0 provides the user with an on-screen display of the Patent Application with the View Work in Progress Window (Figure 3-6).

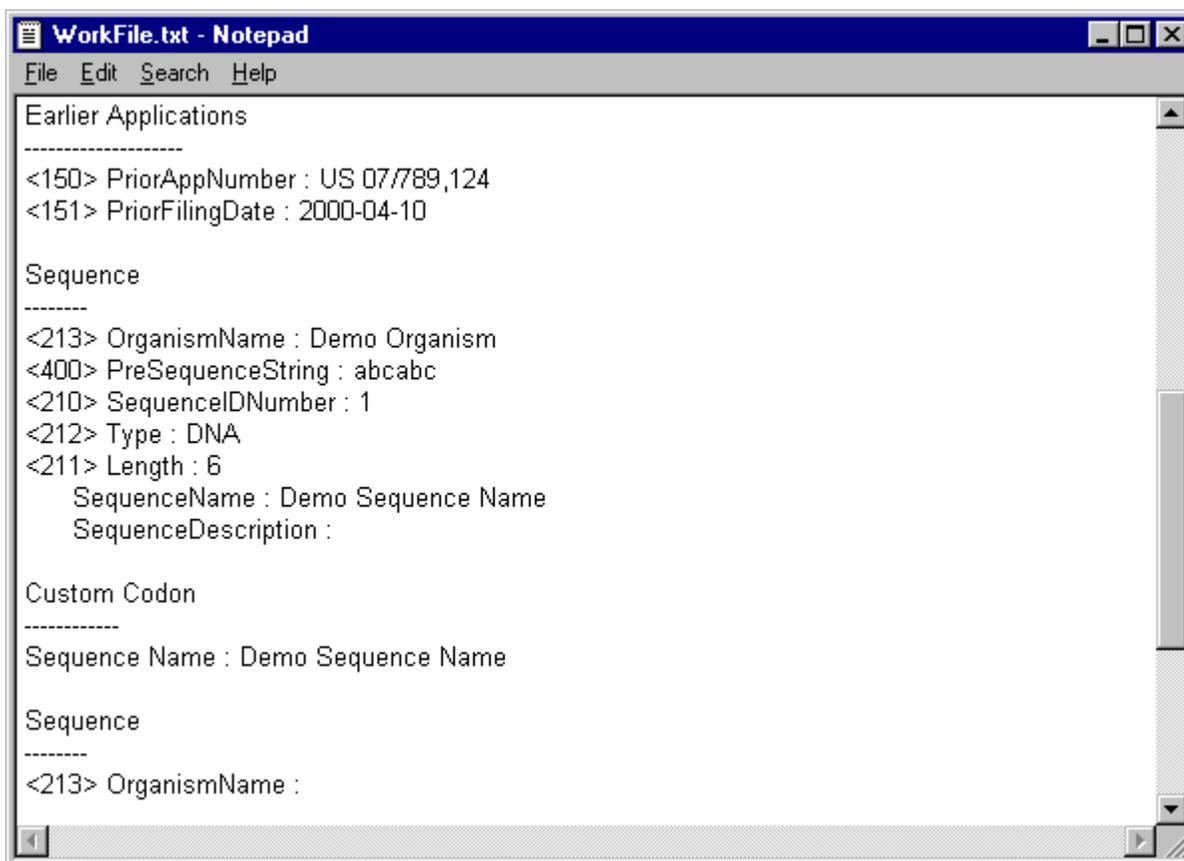


Figure 3-6: View Work in Progress Window

To view the current patent application:

1. From the Project menu,  select View Work in Progress.

2. To print the error report,  click on the File then Print.
3. To exit the screen,  click on File Exit.

 Note: This work file was built from the sequence generation.

3.8 VIEW A SEQUENCE LISTING

PatentIn 3.0 provides the user with an on-screen of the Sequence Listing with the View Sequence Listing Window(Figure 3-7).

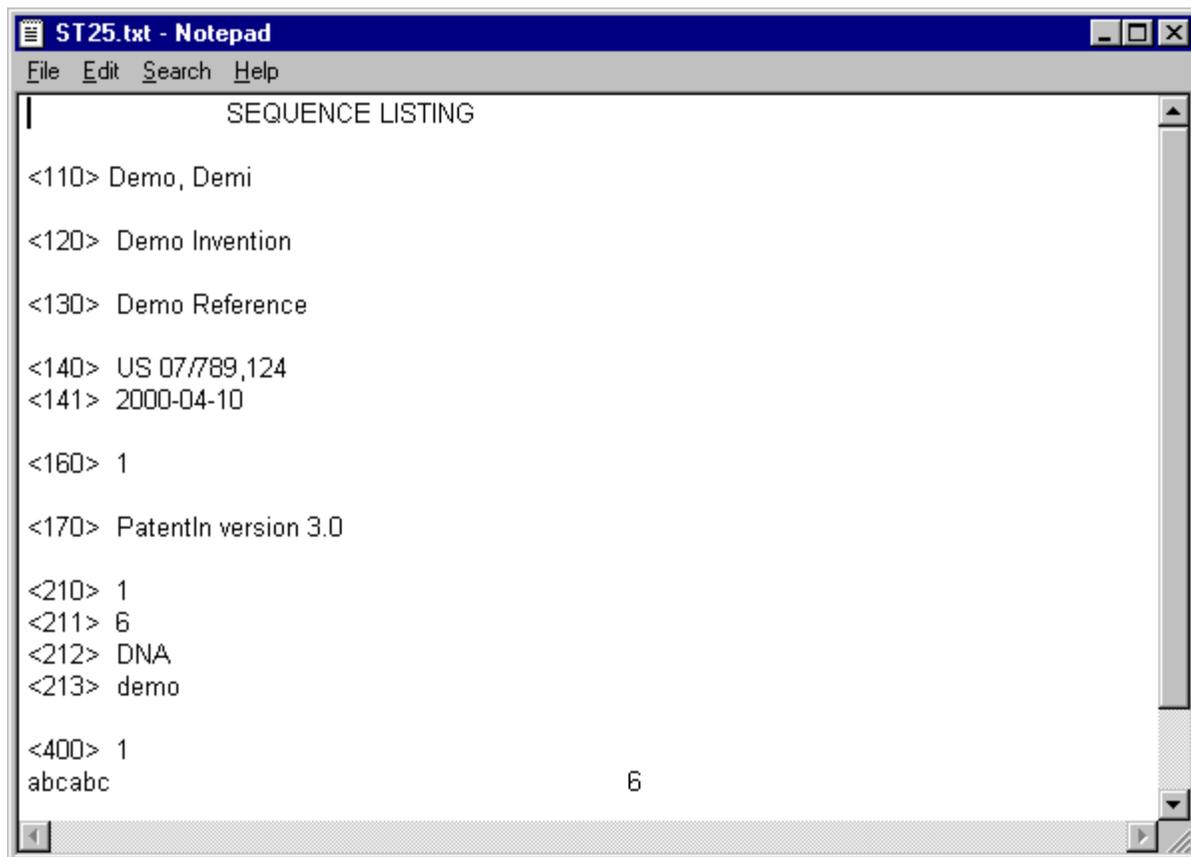


Figure 3-7: View Sequence Listing Window

To view the sequence listing:

1. From the Project menu,  select **View Sequence Listing**.
2. To print the error report,  click on the **File** then **Print**.
3. To exit the screen,  click on **File** then **Exit**.

 Note: The sequence must first be generated.

3.9 VIEWING ERROR REPORTS

PatentIn 3.0 provides the user with an on-screen Error Report with the View Error Report Window(Figure 3-8), if one exists, for the opened project.

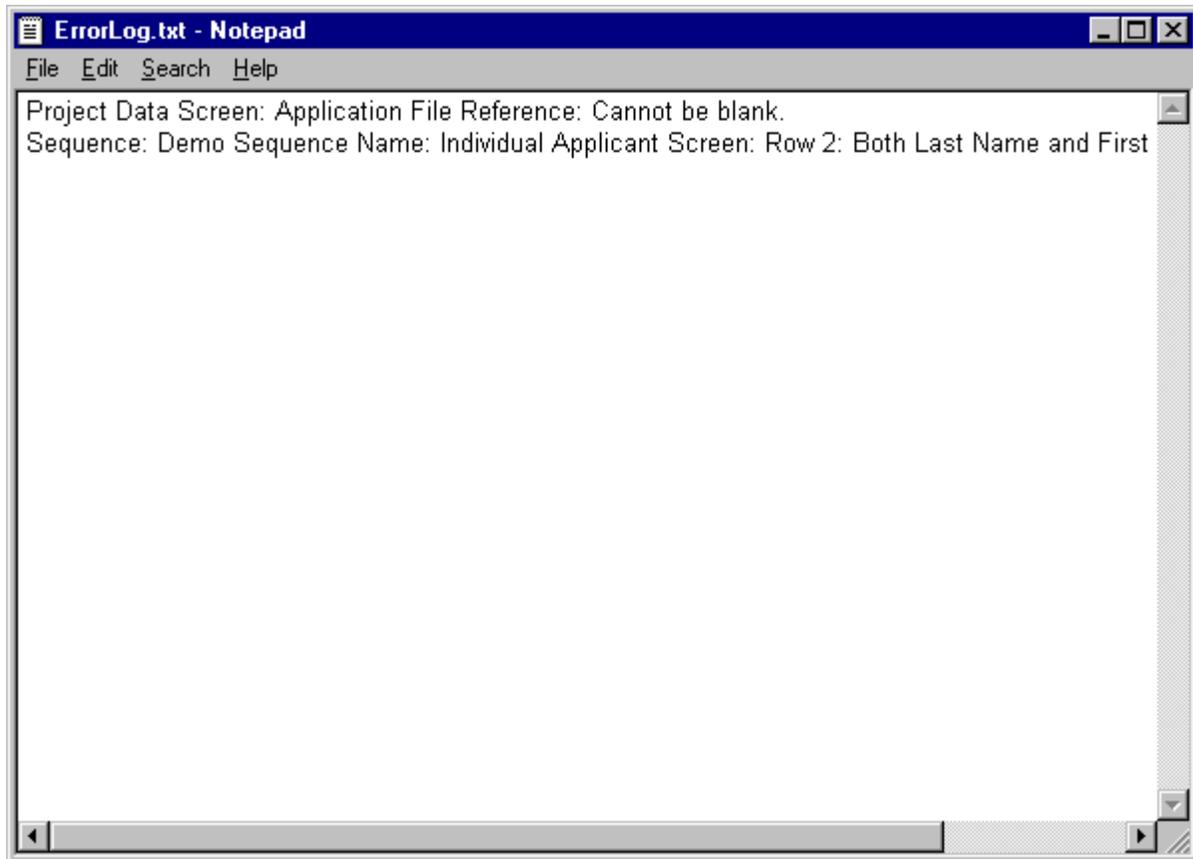


Figure 3-8: View Error Report Window

To view an error report:

1. From the **Project** menu,  select **View Error Report**.
2. To print the error report,  click on the **File** then **Print**.
3. To exit the screen,  click on **File** then **Exit**.

3.10 EXIT PATENTIN 3.0

If the project does not have a current save the user will be queried with the Exit PatentIn 3.0 Screen(Figure 3-9) about whether the project should be saved:

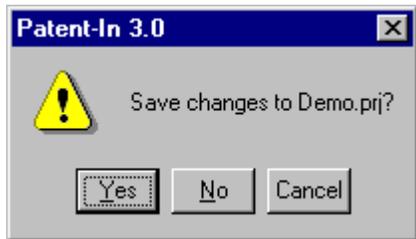


Figure 3-9: Exit PatentIn 3.0 Screen

3.11 HOW TO USE ONLINE HELP

On-line help is available for the PatentIn 3.0 application screens. PatentIn 3.0 Help Screen (Figure 3-10), presents a typical help screen. Pressing the help button on the active screen accesses the on-line help screen.

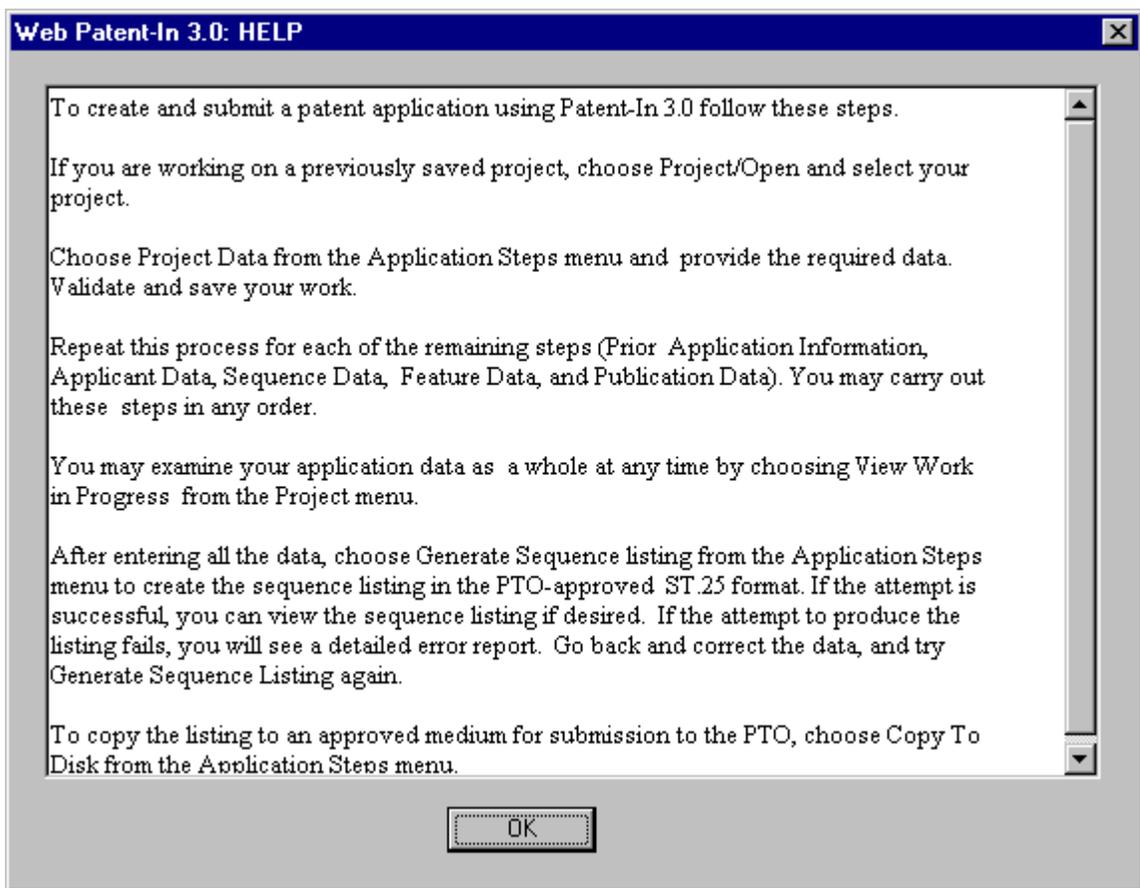


Figure 3-10: PatentIn 3.0 Help Screen

1. To exit the **Help** screen, click on the **OK** button.

3.12 PATENTIN 3.0 MESSAGE DIALOG

The PatentIn 3.0 Message Dialog Screen (Figure 3-11) is a screen that appears if one of the action buttons (Add, for example, described in Section 4, Project and Applicant Data) is pressed and an entry has not been made to the input area of the screen.

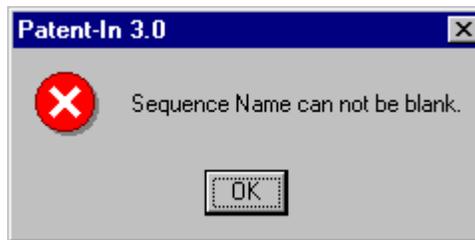


Figure 3-11: PatentIn 3.0 Message Dialog Screen

SECTION 4
PROJECT AND APPLICANT DATA

SECTION 4 PROJECT AND APPLICANT DATA

Once the Sequence Listing data file has been created, the user can add information to the application.

4.1 PATENTIN 3.0 APPLICATION STEPS MENU

The Application Steps Menu (Figure 4-1) selections are available when a project is begun, has been created or selected. The name is visible at the upper left bottom corner of the screen. In this example the project has opened a previously existing file, Demo is shown for the project name.

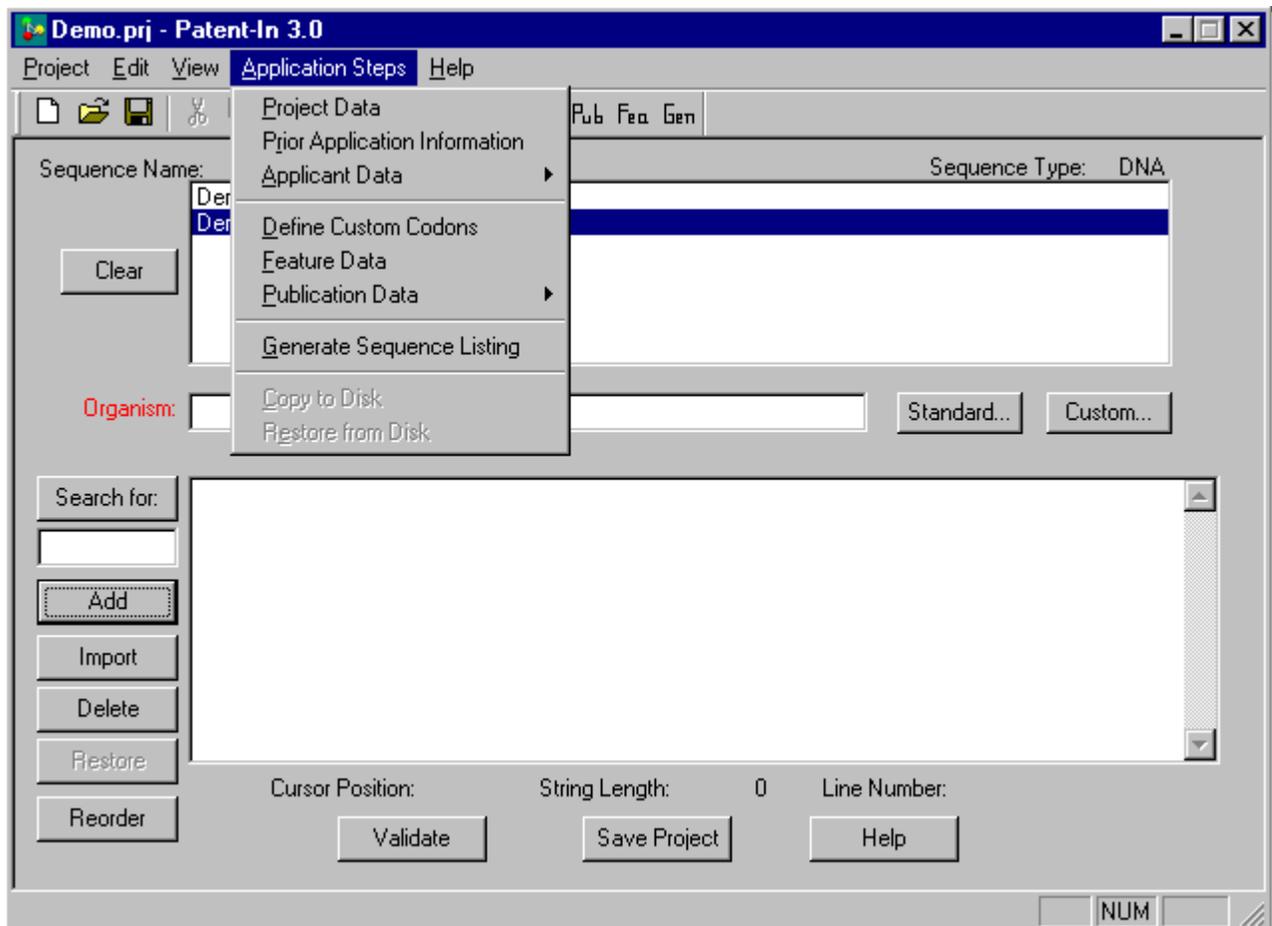
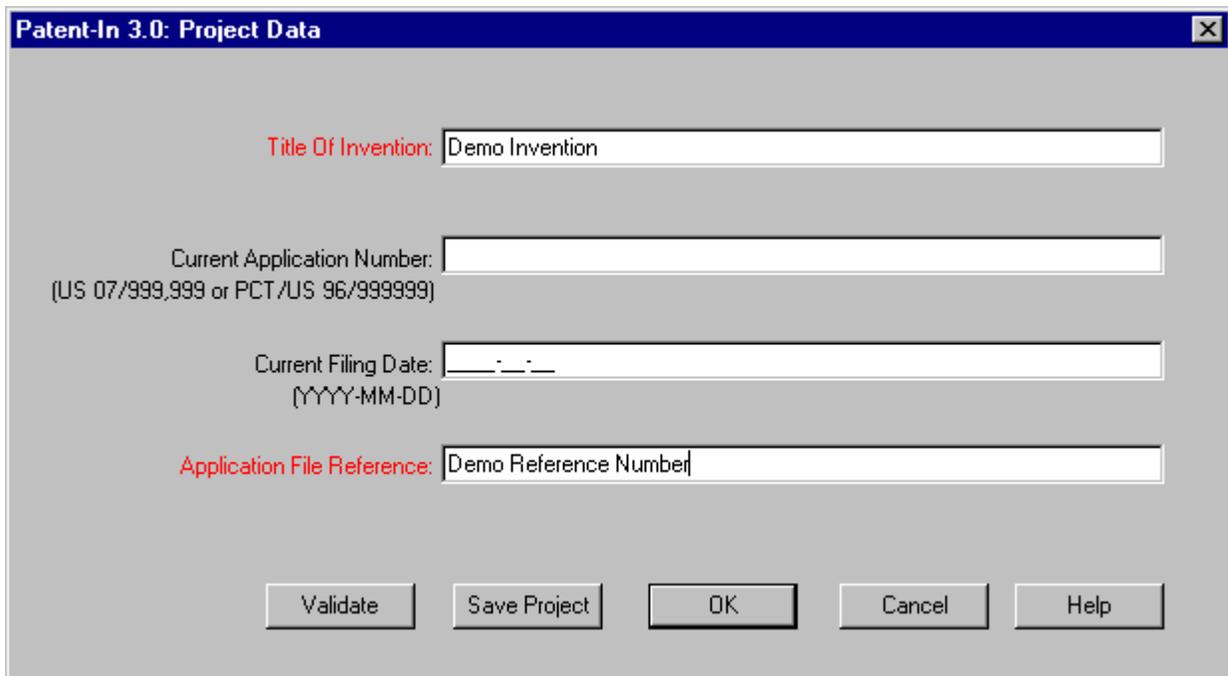


Figure 4-1: PatentIn 3.0 Application Steps Menu

4.2 PROJECT DATA

The PatentIn 3.0 Project Data Screen (Figure 4-2) provides the user with input fields to establish the identifying information for the new invention. This information is the key that establishes the title of the invention and the filing date.



i Note: The mandatory information fields are in red.

Figure 4-2: PatentIn 3.0 Project Data Screen

To enter Project Data:

1.  Enter the **Title of the Invention**. This information is mandatory.
2.  Enter the **Current Application Number**, if one exists. If an application is entered the current filing date becomes mandatory.
3.  Enter the **Current Filing Date**. The date format is numeric: YYYY-MM-DD.
4.  Enter the Application File Reference.
5. To validate the information entered,  click on **Validate**.
6. To save the information,  click on the **Save Project** button.

4.3 PRIOR APPLICATION INFORMATION

Entering information about prior applications is optional. This information will help the patent examiner process the claim. Any number of prior applications may be included on the form. They will be displayed in the table in the order entered and may be selected for editing or deletion (PatentIn 3.0 Prior Application Information Screen).

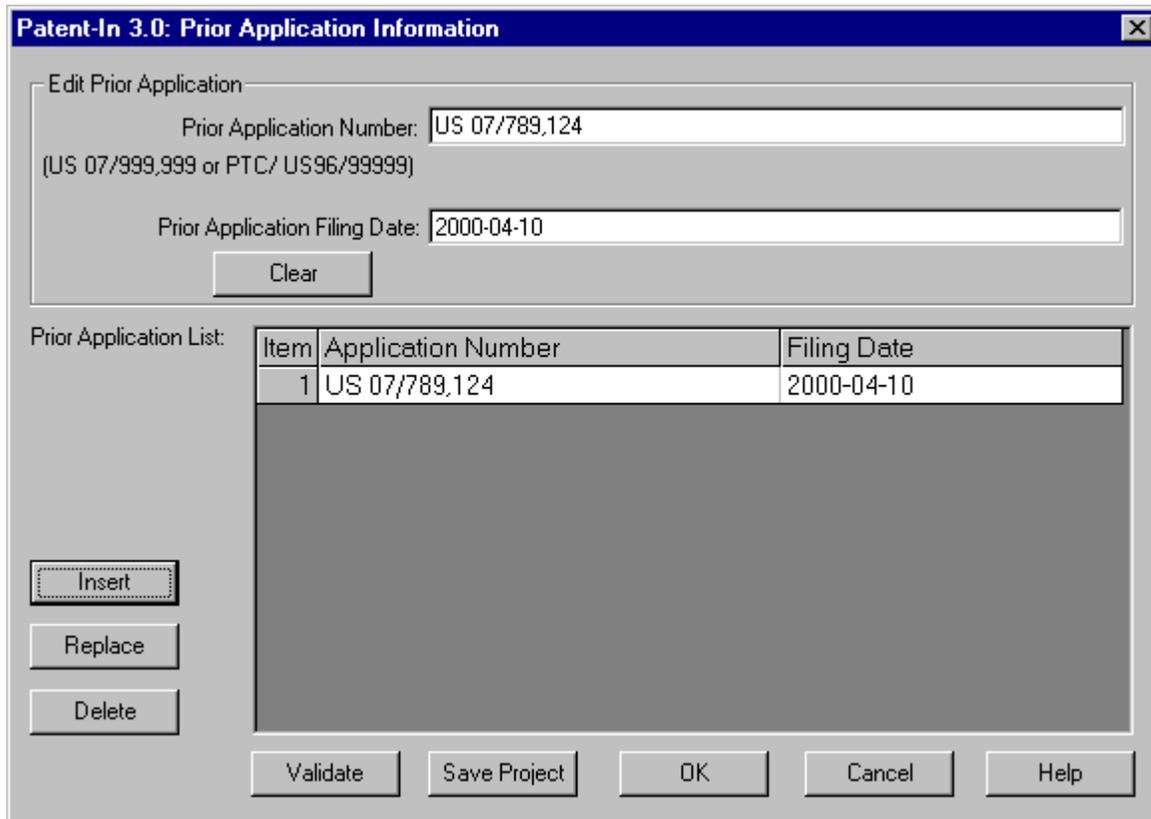


Figure 4-3: PatentIn 3.0 Prior Application Information Screen

To enter information about a Prior Application:

1. Enter the **Prior Application Number**. If a prior application number is entered then the prior application date becomes mandatory.
2. Enter the **Prior Application Filing Date**. The date format is numeric: YYYY-MM-DD.
3. To clear the information in the **Edit Prior Application** area, click on **Clear**.
4. To insert the information to the list, select the item you want the information to follow, enter the **Prior Application Number** and the **Prior Application Filing Date**, then click on the **Insert** button.
5. To replace an entry from the list, select the item, enter the **Prior Application Number** and the **Prior Application Filing Date**, then click **Replace**.
6. To delete an entry from the list, select the item from the list, and then click on the **Delete** button.
7. To validate the information entered, click on **Validate**. Data entered in the table (Insert) is then validated. Information in the edit area, that has not yet been inserted, is not validated.
8. To save the information, click on the **Save Project** button.
9. To validate and close, click on the **OK** button.

4.4 APPLICANT DATA

The Applicant Data Screen (Figure 4-4) allows the user to input screen for an Individual or Organizational applicant. Select Applicant Data from the Application Steps menu, then select either Individual or Organization from the next menu. If Individual is selected, the PatentIn 3.0 Individual Applicant Screen (Figure 4-5) will appear. If Organization is selected, the PatentIn 3.0 Organization Applicant Screen (Figure 4-6) will appear.

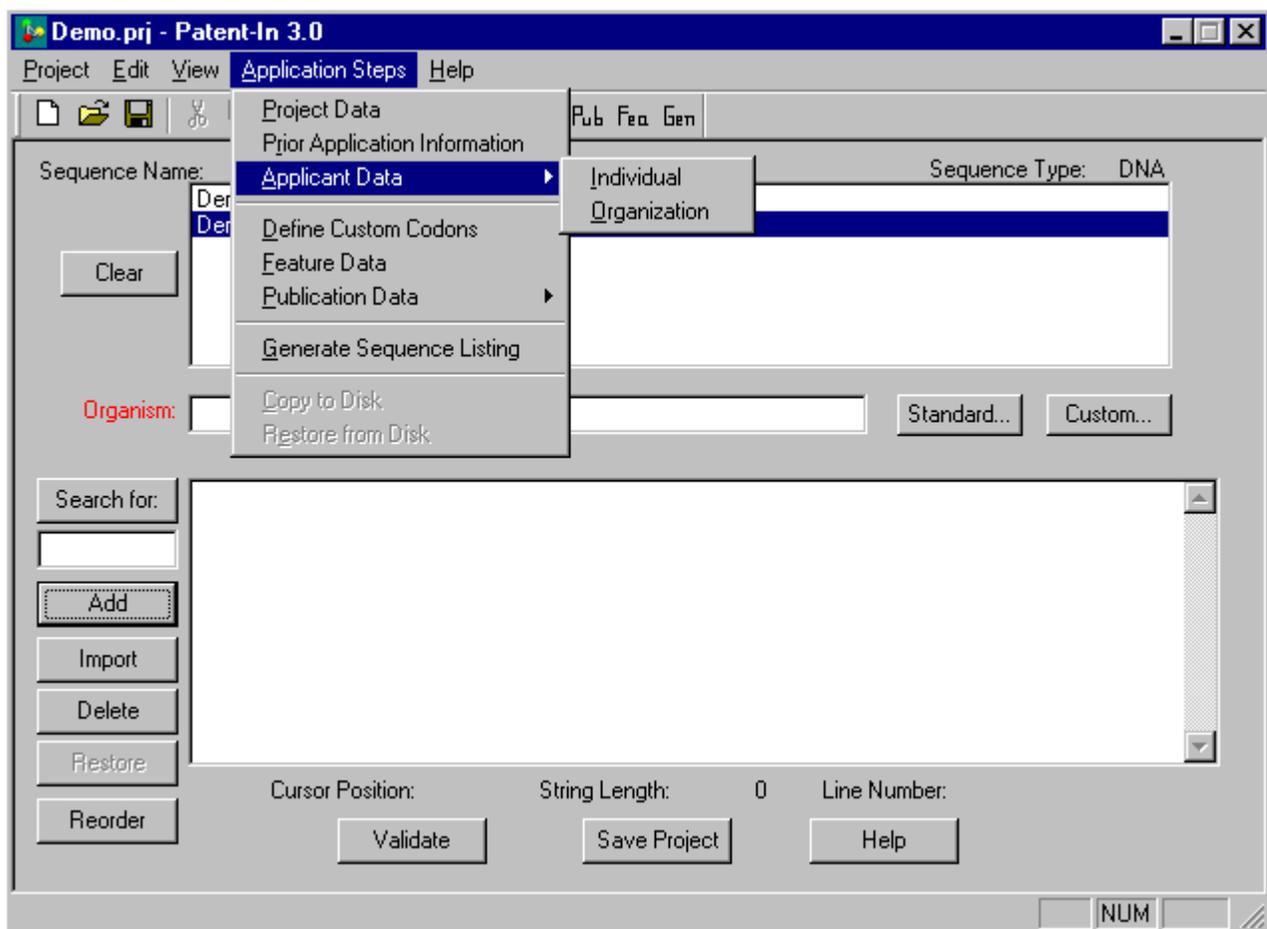


Figure 4-4: Applicant Data Screen

4.4.1 Individual Applicant

The PatentIn 3.0 Individual Applicant Screen (Figure 4-5) allows the user to enter information about an individual applicant.

i Note: The field names in red (Last Name and First Name) are mandatory information.

The screenshot shows a software window titled "Patent-In 3.0: Individual Applicant". The window is divided into two main sections. The top section is titled "Edit Individual Applicant" and contains several input fields: "First Name:", "Last Name:", "Suffix:", "Middle Initial:", "Street Address:", "City:", "State / Province:", "Country:", "Zip Code:", "Phone Number:", "Fax Number:", and "Electronic Mail Address:". There is a "Clear" button next to the "City" field. The bottom section is titled "Applicant List:" and contains a table with three columns: "Item", "Individual Name", and "Phone Number". Below the table are three buttons: "Insert", "Replace", and "Delete". At the bottom of the window are five buttons: "Validate", "Save Project", "OK", "Cancel", and "Help".

Figure 4-5: PatentIn 3.0 Individual Applicant Screen

To enter information about an Individual Applicant:

1. From the Application Steps menu, Select Applicant Data, then Select Individual.
2. Enter the User's Last Name (surname).
3. Enter any Suffix the user has on his/her name (e.g., Jr., III).
4. Enter the User's First Name.
5. Enter the User's Middle Initial.
6. Enter the User's Street Address, City, State/Province, Country, Zip/Postal Code, Phone Number, Fax Number, and Electronic Mail Address.
7. To clear the information about the Individual Applicant click on **Clear**.
8. To insert the information to the list, select the item you want the information to follow, enter the **Edit Individual Applicant** information, then click on the **Insert** button.
9. To replace an entry from the list, select the item, enter the **Edit Individual Applicant** information, and then click Replace.
10. To delete an entry from the list, select the item from the list, and then click on the **Delete** button.

11. To validate the information entered,  click on **Validate**. Data entered in the table (Insert) is then validated. Information in the edit area, that has yet been inserted, is not validated.
12. To validate and close,  click on the **OK** button.
13. To add another applicant to the list repeat Steps 1-12.

4.4.2 PatentIn 3.0 Organization Applicant

The PatentIn 3.0 Organization Applicant Screen (Figure 4-6) allows the user to enter information about an organization applicant.

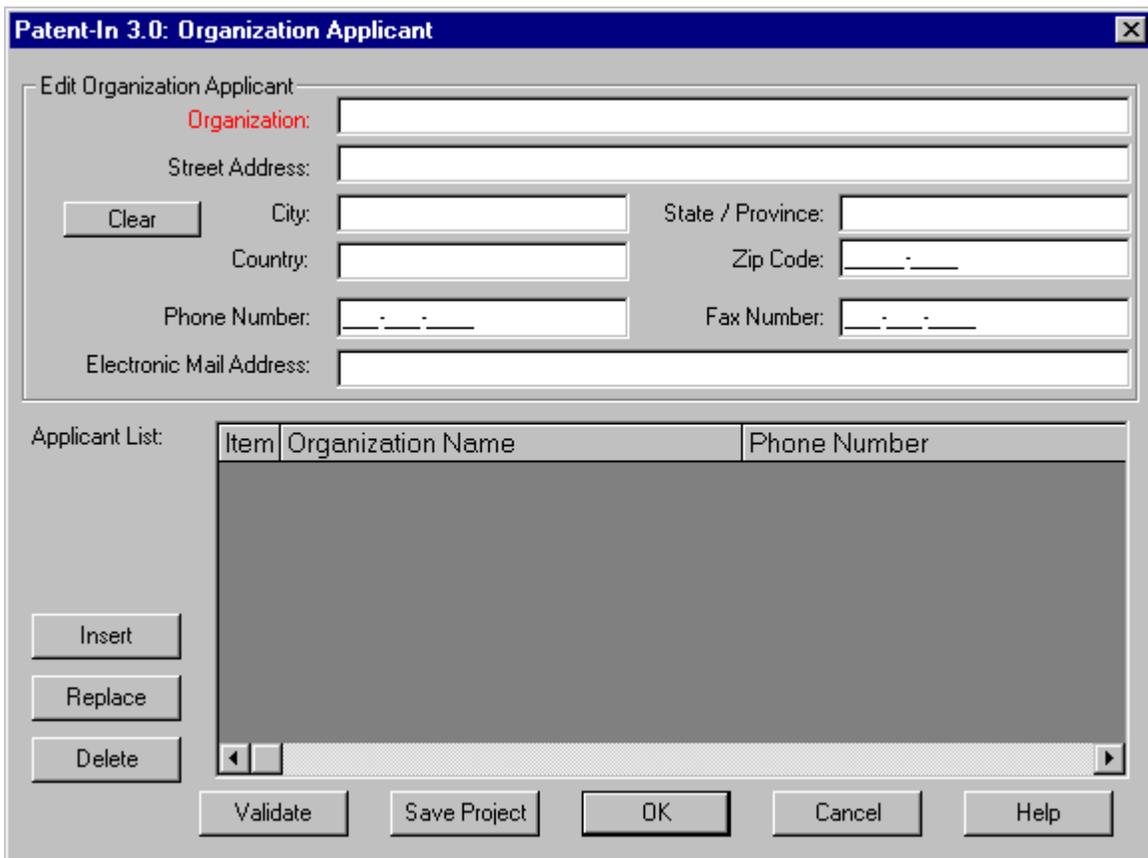


Figure 4-6: PatentIn 3.0 Organization Applicant Screen

To enter information about an Organization Applicant:

1. From the **Applicant Steps** menu,  Select **Applicant Data**, then  Select **Organization**.
2. Enter the **Organization's** Name.
3. Enter the Organization's Street Address, City, State/Province, Country, Zip/Postal Code, Phone Number, Fax Number, and Electronic Mail Address.
4. To clear the information about the Edit Organization Applicant portion of the screen,  click on **Clear**.

5. To insert the information to the list,  select the item you want the information to follow,  enter the **Edit Organization Applicant** information, then  click on the **Insert** button.
6. To replace an entry from the list,  select the item,  enter the **Edit Organization Applicant** information, and then  click **Replace**.
7. To delete an entry from the list,  select the item from the list, and then  click on the **Delete** button.
8. To validate the information entered,  click on **Validate**. Data entered in the table (Insert) is then validated. Information in the edit area, that has not yet been inserted, is not validated.
9. Repeat steps 2 through 9 until all applicant information has been included.
10. To validate and close,  click on the **OK** button.

SECTION 5
SEQUENCE DATA

SECTION 5 SEQUENCE DATA

5.1 SEQUENCE

The Sequence Screen (Figure 5-1) you to create and modify sequences. You can create and edit custom codons and custom organism names from this screen. It also provides a search function where a genetic sequence may be entered and searched for in the files on his workstation. The user will access this screen immediately after PatentIn 3.0 is started or by selecting Create User Work File from the Project menu.

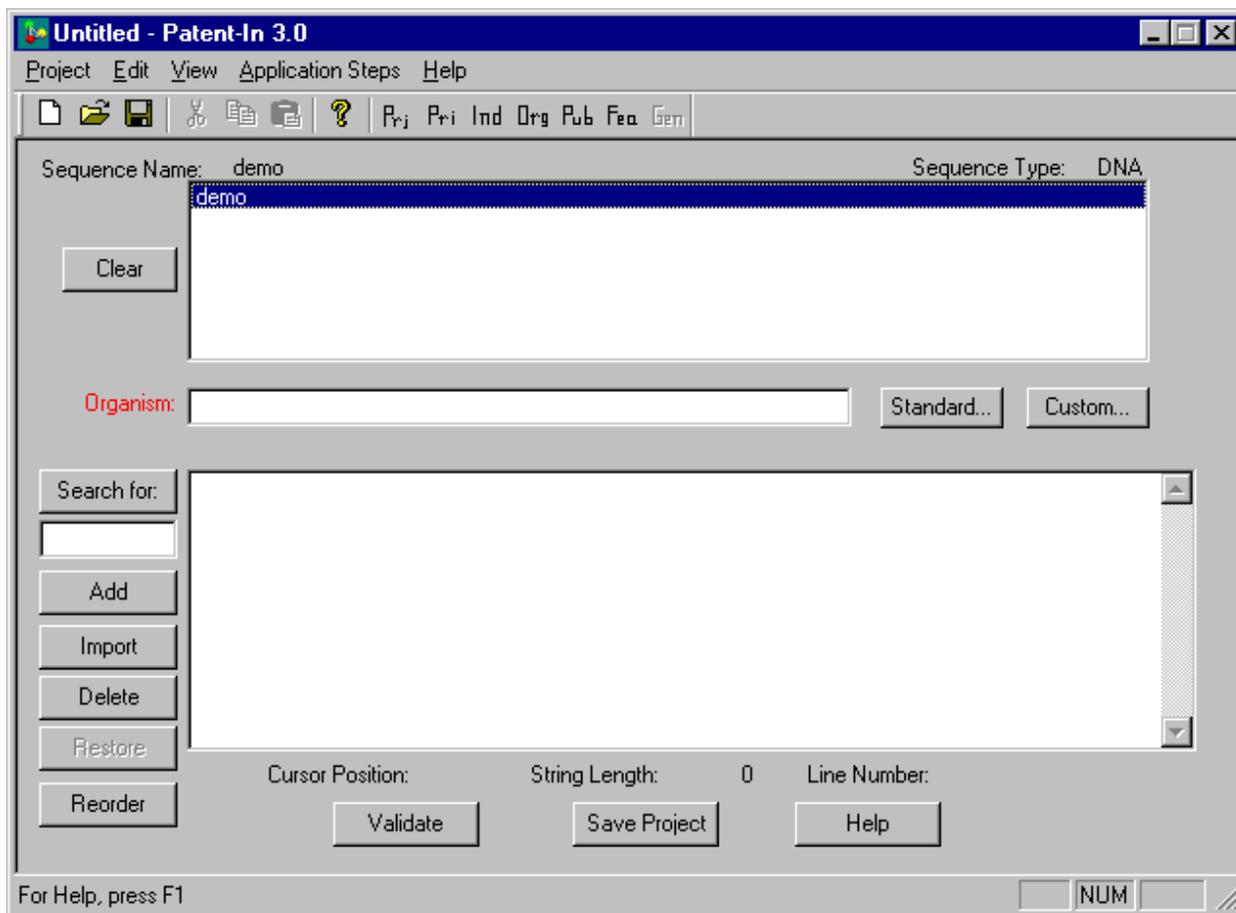


Figure 5-1: Sequence Screen

To select a sequence for editing:

- ☞ Select the sequence name from the list of sequences.

The following sequence characteristics are displayed:

Cursor Pos Shows the current cursor position.

String Length Shows the length of the sequence string on the line.

Line Number Indicates the line number of the cursor relative to the beginning of the string.

5.1.1 Selecting a Standard **Organism**

This screen enables the user to select an organism name from common organisms. Included in its capabilities is an attempt matches on partially input names.

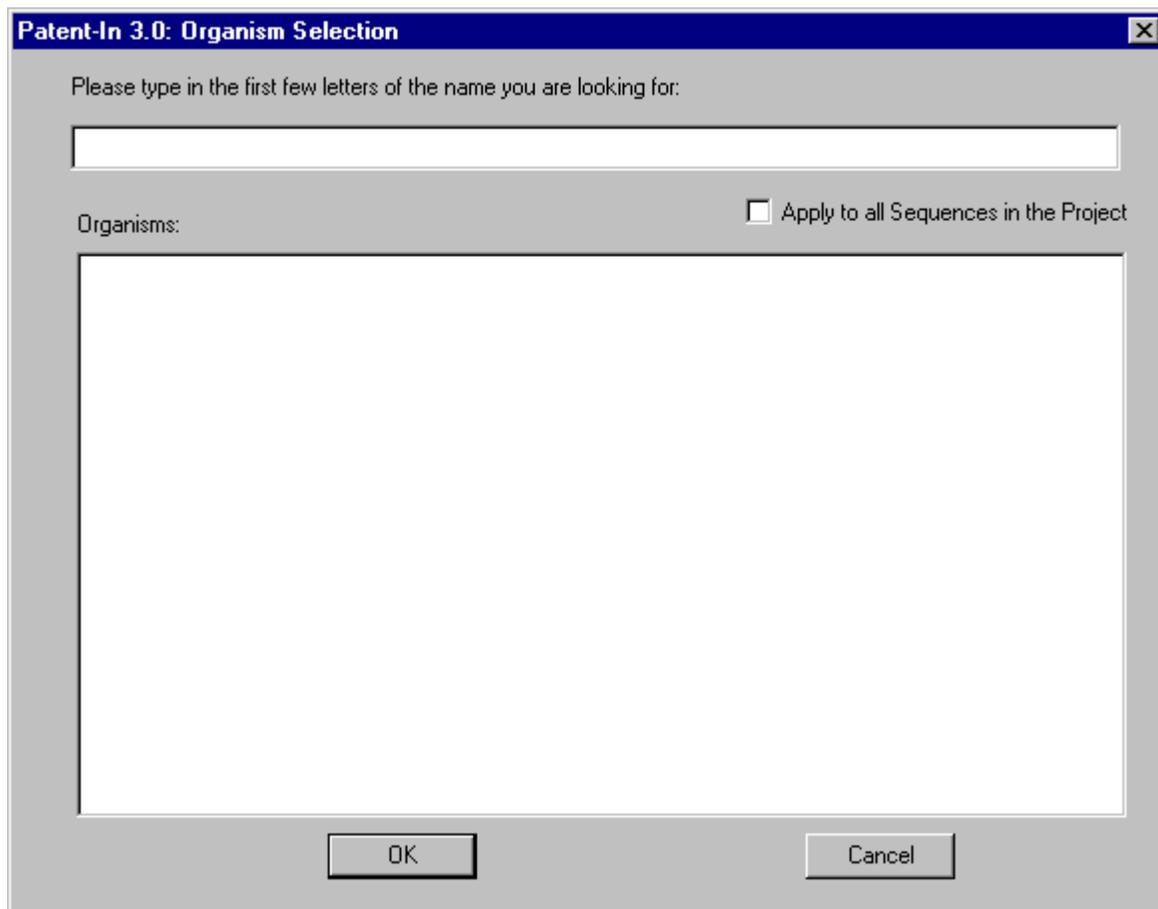


Figure 5-2: Selecting a Sequence Number Screen

To select an Organism Name:

1.  Click on the **Standard** button.
2.  Begin entering characters for the organism you are looking for.
3.  Click on the OK button to enter the selected organism name.

5.1.2 Searching for a Sequence

To search for a specific sequence:

1.  Enter a particular substring (a feature, for example) in the edit field below the **Search for** button.
2.  Click on the **Search** button. The cursor will move the first instance of that sub-sequence.

 **NOTE:** Each search is limited/truncated to 60 characters.

5.1.3 Clearing the Screen

1. To clear the entire screen,  Click on the **Clear** button (Figure 5-1).

5.2 ADDING A SEQUENCE

The **Add** button on the Sequence Screen (Figure 5-1) provides a means to enter a sequence name and to select a sequence type from a list of radio buttons (Figure 5-3).

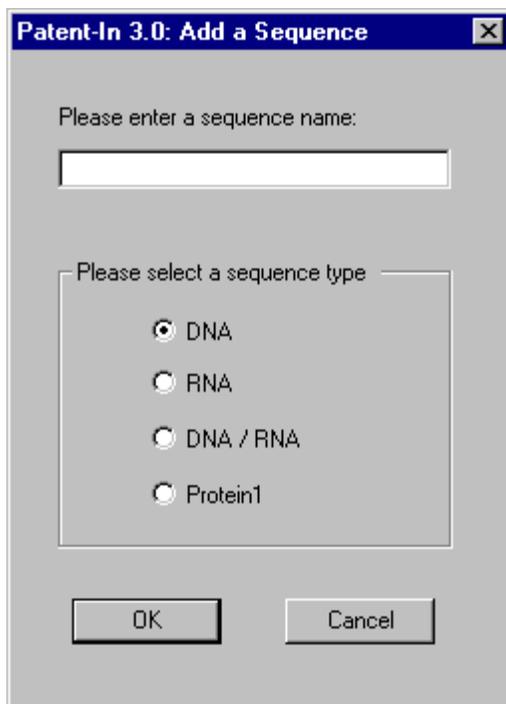


Figure 5-3: PatentIn 3.0 Add A Sequence Screen

To add a sequence:

1. From the Sequence screen,  select the **Add** button. The PatentIn 3.0 Add A Sequence Screen appears.
2.  Enter the sequence name into the dialog box.
3.  Select the sequence type by clicking on the  radio button next to the appropriate sequence type.

You can now enter sequence strings in the edit field at the bottom of the screen. If you are using Windows 95, a maximum of 64K characters will display in the field. In Windows NT and 98, the upper limit is over 1 million sequence characters.

You can work around these limitations by using import files, rather than the Sequence Editor, to create and edit sequences.

5.2.1 Importing a Sequence

The **Import** button on the Sequence screen (Figure 5-1) provides a means to import a sequence name and then to select an import source from two radio buttons.

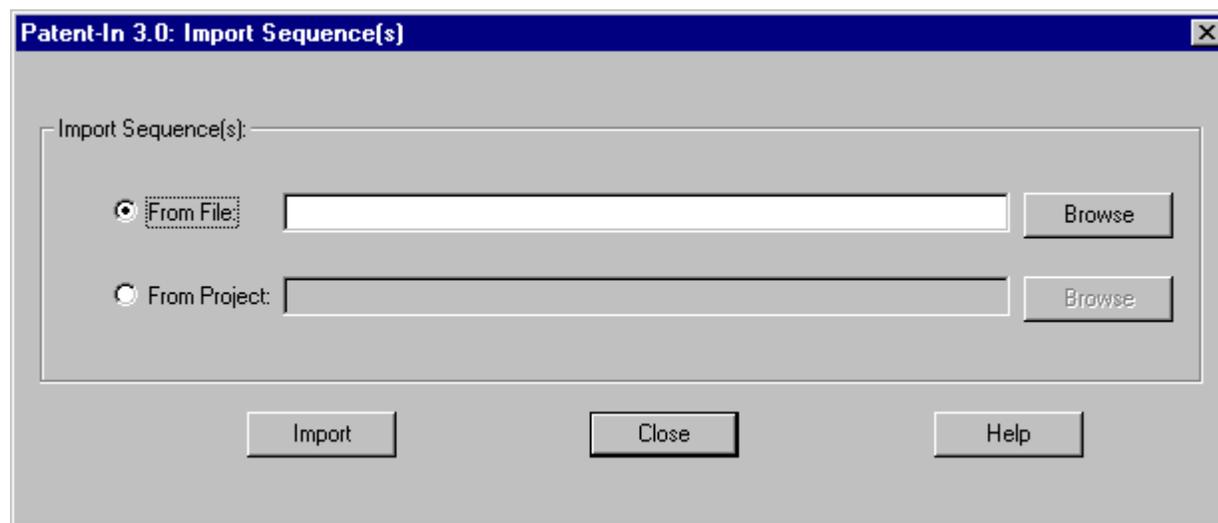


Figure 5-4: Import Sequence(s) Screen

1. To use a sequence from a text file,  click on the **Import Sequence** button, then  click on the **From File** radio button. (See 5.2.2)
2. To use a sequence from another project,  click on the **Import Sequence** button, then  click on the **From Project** radio button.
3. A **Browse** button is provided to assist the user in providing the file folder and file name.

 **NOTE:** For the Protein/3 selection, the data must be imported from a text file that contains only amino acid abbreviated names as shown in Appendix D: Exchange Nucleotide Characters and Amino Characters, PRT/3 Column. The PRT/3 strings are converted to PRT/1 characters for subsequent use in the Sequence Editor.

5.2.2 Format for Sequence Data Files to be Imported by PatentIn 3.0

A sequence file is an ASCII text file containing one or more sequences. Each sequence begins with a header having the following format. The header must be the first non-blank text on its line.

5.3 COPYING A SEQUENCE

PatentIn uses standard Windows type edit features.

To copy a sequence:

1.  Highlight the sequence to be copied.
2.  Click on the **Edit** menu then  Click **Copy**. (Figure 5-6)

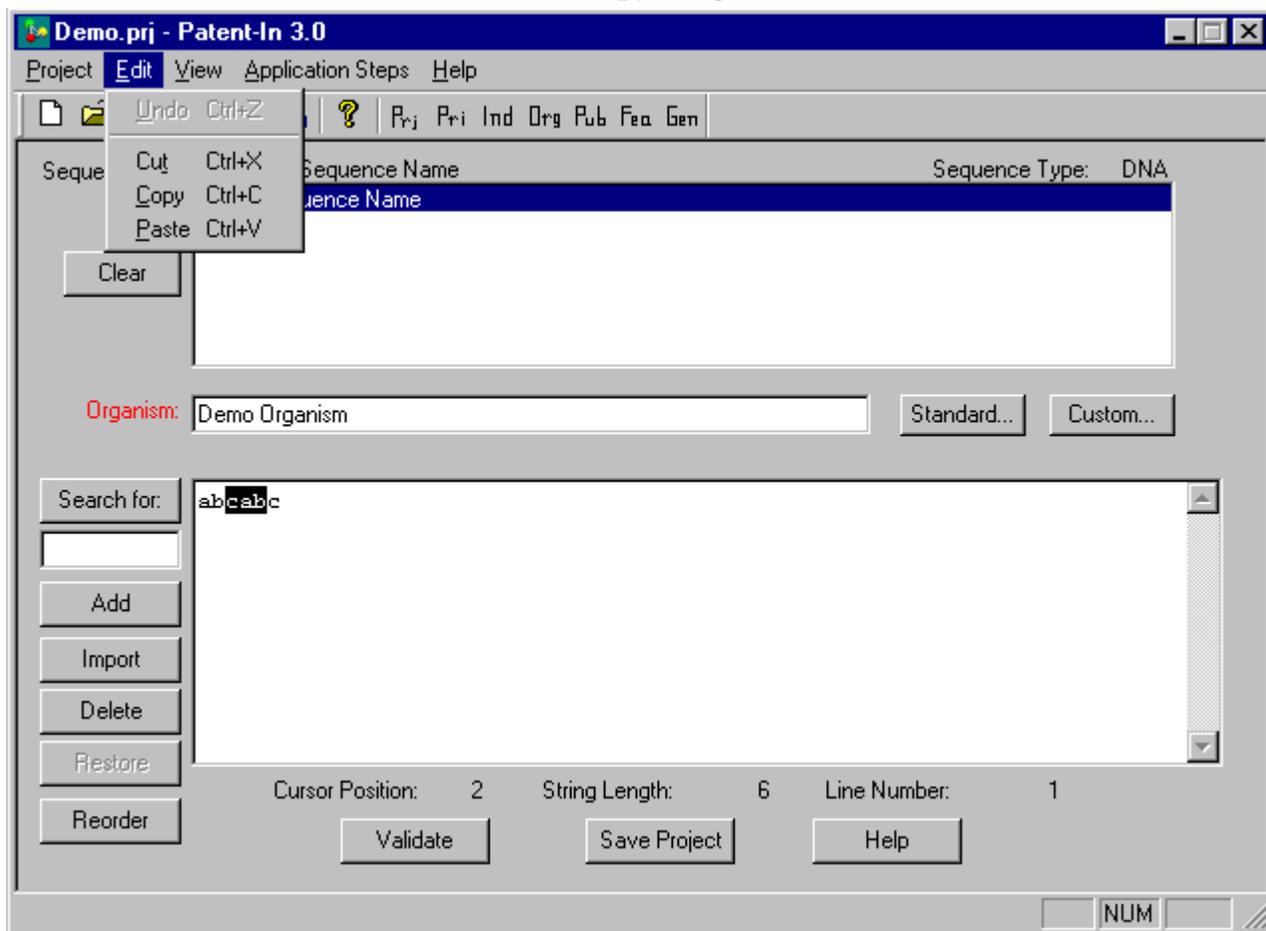


Figure 5-6: Edit Menu

5.4 PASTING A SEQUENCE

To paste a sequence:

1. Position the cursor where the copied material is to be inserted.
2.  Click on the **Edit** then  Click **Paste**.

5.5 DELETING A SEQUENCE

To delete a sequence:

1.  Click on the **Delete** button.

5.6 RESTORING A SEQUENCE

When a sequence has been deleted it can be restored until the current project update is terminated.

To restore a sequence:

1.  Click on the **Restore** button on the main screen. The Sequence Recovery Screen (Figure 5-7) appears.
2.  Select the sequence(s) to be restored.
3.  Click on the **Restore** button.

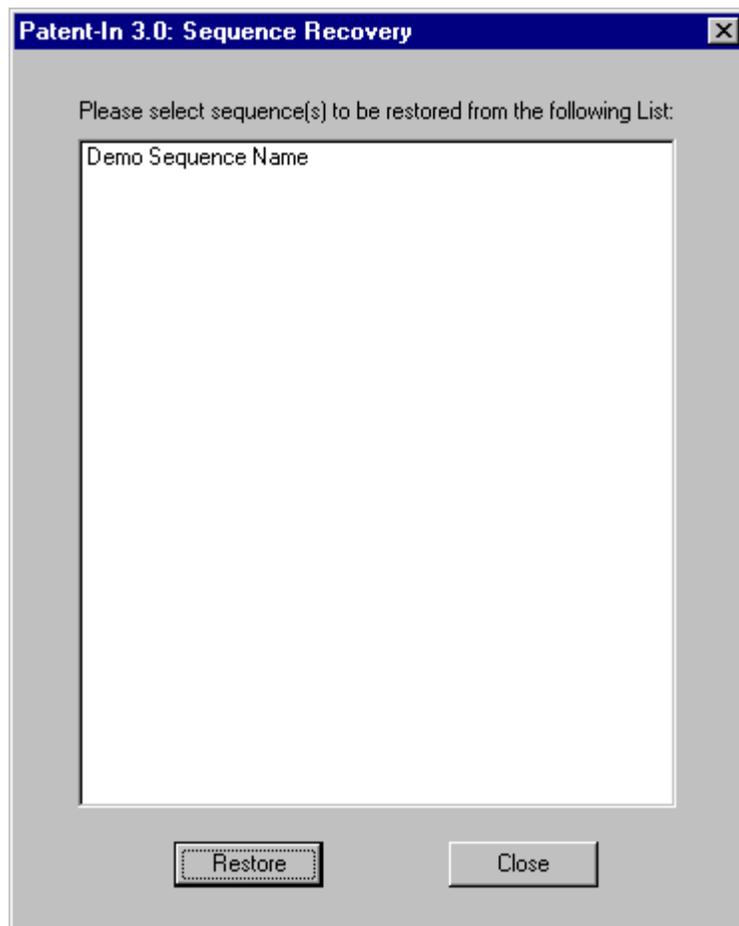


Figure 5-7: Sequence Recovery Screen

5.7 REORDERING SEQUENCES

The PatentIn 3.0 Reorder Sequences Screen (Figure 5-8) provides the user with the means to compare the current sequence order and the new sequence order. The Current Sequence Order displays the sequences in the order that the sequences were entered into the application. The New Sequence Order displays the sequences in the order that the user specifies by using the Add and Remove buttons.

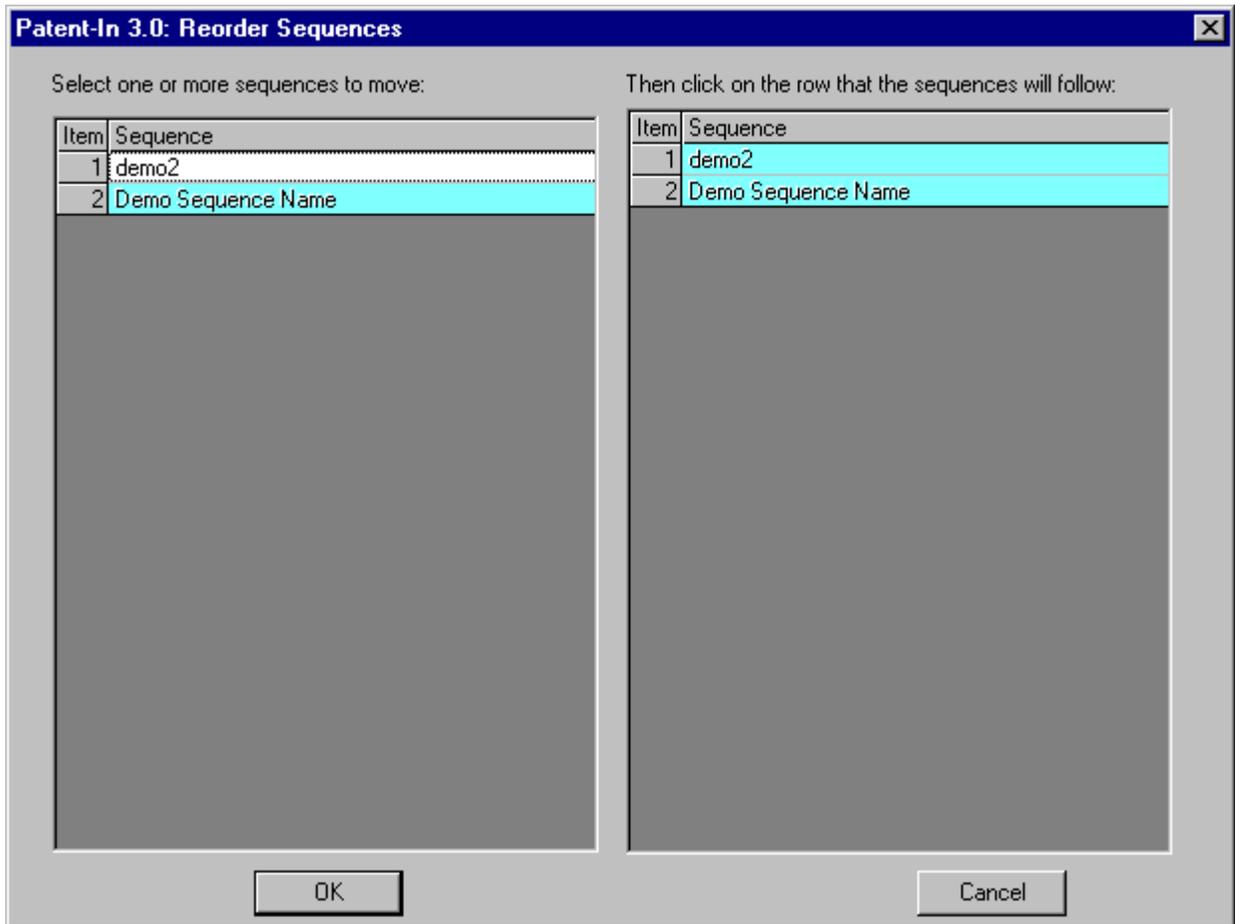


Figure 5-8: PatentIn 3.0 Reorder Sequences Screen

To reorder sequences:

1. Select the sequences from the menu on the left-hand side.
2. Click on the row the sequence will follow.
3. Repeat steps 1-2 until the sequences are in the desired order.

5.8 VALIDATING SEQUENCES

To Validate the Sequences:

1. On the Sequence Screen (Figure 5-1), Click on the **Validate** button. A message screen will inform you if there was an error, otherwise Validation OK will appear on the status bar.

NOTE: FOR THE SEQUENCE DATA, VALIDATION IS DONE FOR THE SELECTED SEQUENCE NAME.

5.9 SAVING SEQUENCES

To Save a Sequence:

1. On the Sequence Screen (Figure 5-1), Click on the **Save** button. Your work will be saved in its current state.

5.10 ADDING CUSTOM CODONS

The PatentIn 3.0 Custom Codon Input Screen (Figure 5-9) provides the means to add Custom Codons to the list of standard codons on the user workstation. This screen is accessed from the Application Steps menu (Figure 4-1) by selecting the Define Custom Codon item.

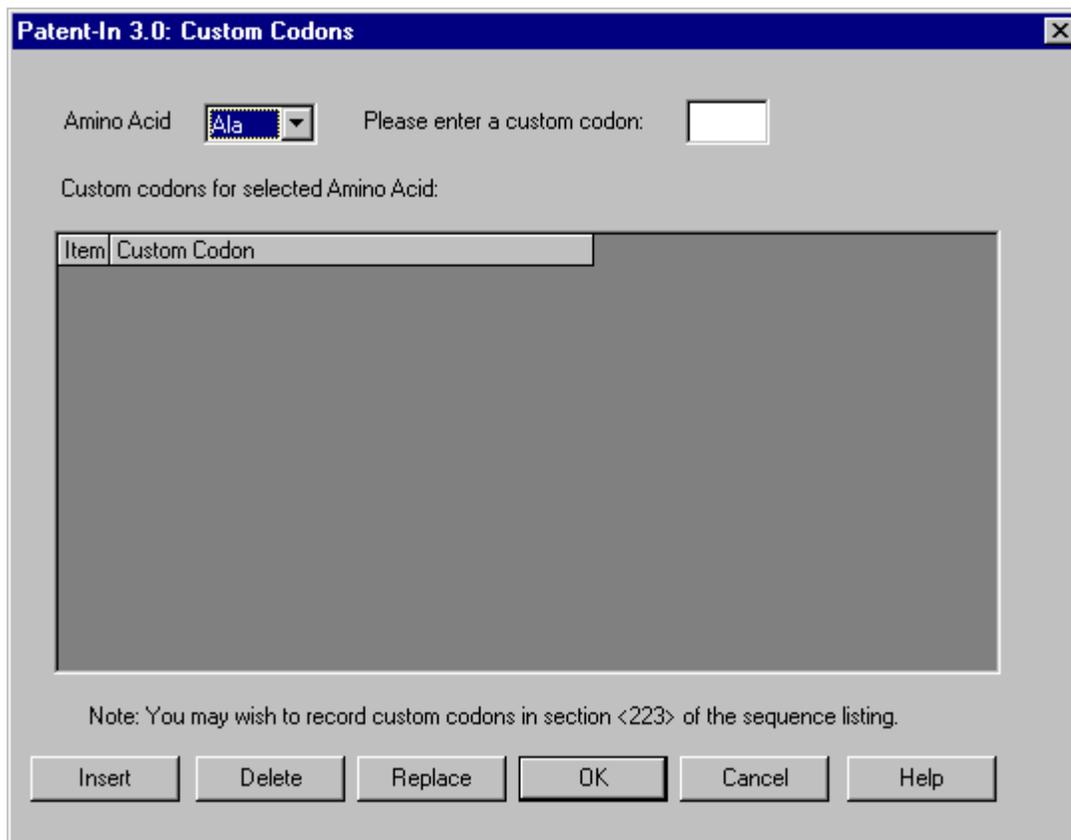


Figure 5-9: PatentIn 3.0 Custom Codon Input Screen

To add a Custom Codon:

1.  Select the **Define Custom Codon** item from the **Application Steps** menu (Figure 4-1).
2.  Select an **Amino Acid** from the drop-down list (Figure 5-10).
3.  Enter the **Custom Codon**.
4.  Click on the **Insert** button.

To delete a Custom Codon:

1. Click on the Custom Codon in the list.
2. Click on the **Delete** button.

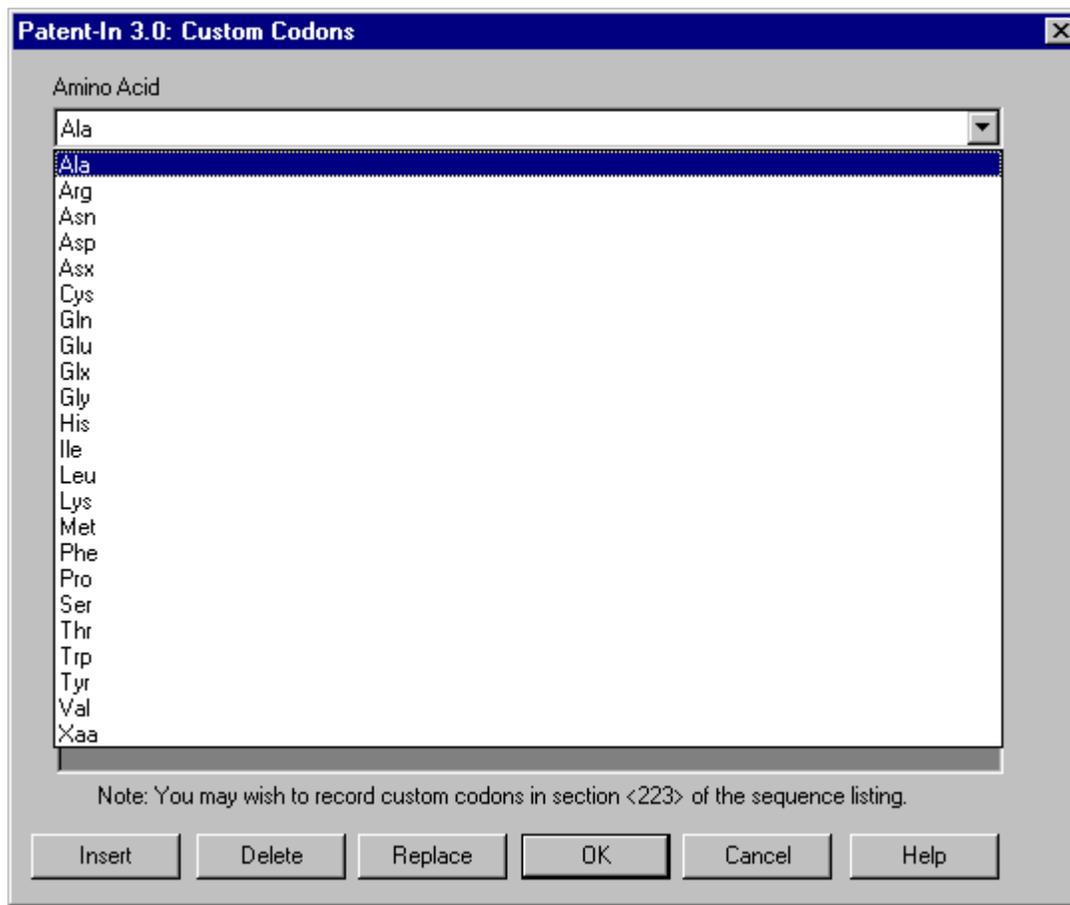


Figure 5-10: Amino Acid Drop Down List Screen

5.11 ADDING A CUSTOM ORGANISM

The PatentIn 3.0 Custom Organism Input Screen (Figure 5-11) provides the means to add a Custom organism to the list of custom organisms. It also enables you to select a custom organism to enter on the Sequence screen. This screen is accessed from the Sequence screen (Figure 5-1) by selecting the **Custom** button. The user enters the custom organism into the screen, and then can manipulate the list by adding or deleting organisms.

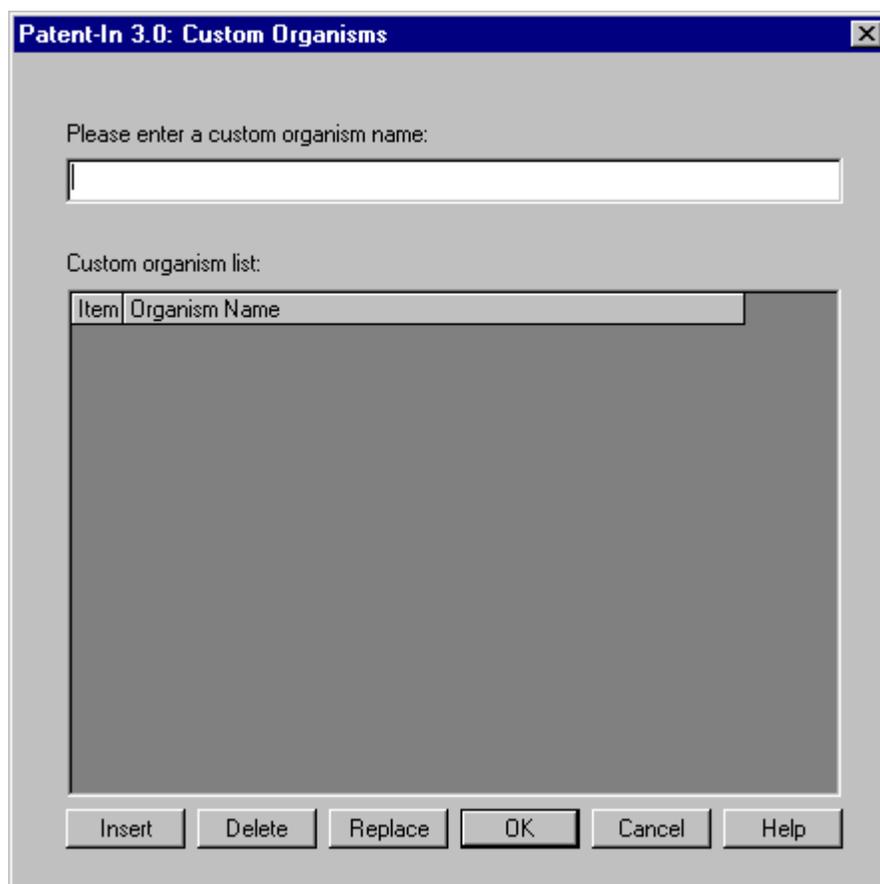


Figure 5-11: PatentIn 3.0 Custom Organism Input Screen

To add a Custom Organism:

1. Select the **Custom** button from the Sequence screen.
2. Enter the Custom Organism.
3. Click on the **Insert** button.

To delete a Custom Organism:

1. Click on the Custom Organism in the list.
2. Click on the **Delete** button.

To replace a Custom Organism:

1. Click on the Custom Organism in the list.
2. Enter the Custom Organism.
3. Click on the **Replace** button.

To enter a Custom Organism on the Sequence screen:

1. Select the Organism so that the name appears in the “Please enter a custom organism name:” box.
2. Click on the **OK** button.

SECTION 6
FEATURE DATA

SECTION 6 FEATURE DATA

6.1 SEQUENCE FEATURES

The PatentIn 3.0 Features Screen (Figure 6-1) enables you to create and modify features pertaining to a sequence. You can access this screen by selecting **Feature Data** from the PatentIn 3.0 Application Steps Menu (Figure 4-1). The features that are displayed apply to the sequence that is currently selected on the Sequence screen.

Patent-In 3.0: Features - demo

Sequence Type: DNA Sequence String Length: 6

Edit Feature

Join All CDSs

Feature Name / Key: Names

Relevant Residues From: To:

Other Information:

Clear

(If you have "n" or "X" in the sequence, please define them in the Other Info. field.)

Feature List:

Item	Feature Name	From Column	To Column
------	--------------	-------------	-----------

Insert

Replace

Delete

Validate Save Project OK Cancel Help

Figure 6-1: PatentIn 3.0 Features Screen

To enter information about a Feature:

1. Check the **Join All CDSs** box if the sequence contains more than one CDS and the CDSs are to be joined.
2. Click on the **Names** button to access the list of Nucleotide Names for **Feature Name / Key**. For more information, see section 7.1.1.

3.  Enter the “**Relevant Residue From**” and “**To**” sequence position numbers.
4.  Click in the **Other Information** box to provide other information. This is where you document X in a protein sequence or n in a base sequence.
5. To clear the **Edit Feature** portion of the screen  Click on the **Clear** button.
6. To insert an entry from the **Feature List**, highlight it and  click on the **Insert** button.
7. To replace an entry from the **Feature List**, highlight it and  click on the **Replace** button.
8. To delete an entry from the **Feature List**, highlight it and  click on the **Delete** button.
9. To validate the information entered,  click on **Validate**. Data entered in the table (Insert) is then validated. Information in the edit area, that has not yet been inserted, is not validated.
10. To save the information,  click on the **Save Project** button.
11. To validate and close,  click on the **OK** button.
12. To cancel the information,  click on the **Cancel** button.
13. To access the help information,  click on the **Help** button.

6.1.1 Feature Key Selection

The Feature Key Selection Screen (Figure 6-2) allows the user to select a Nucleotide name.

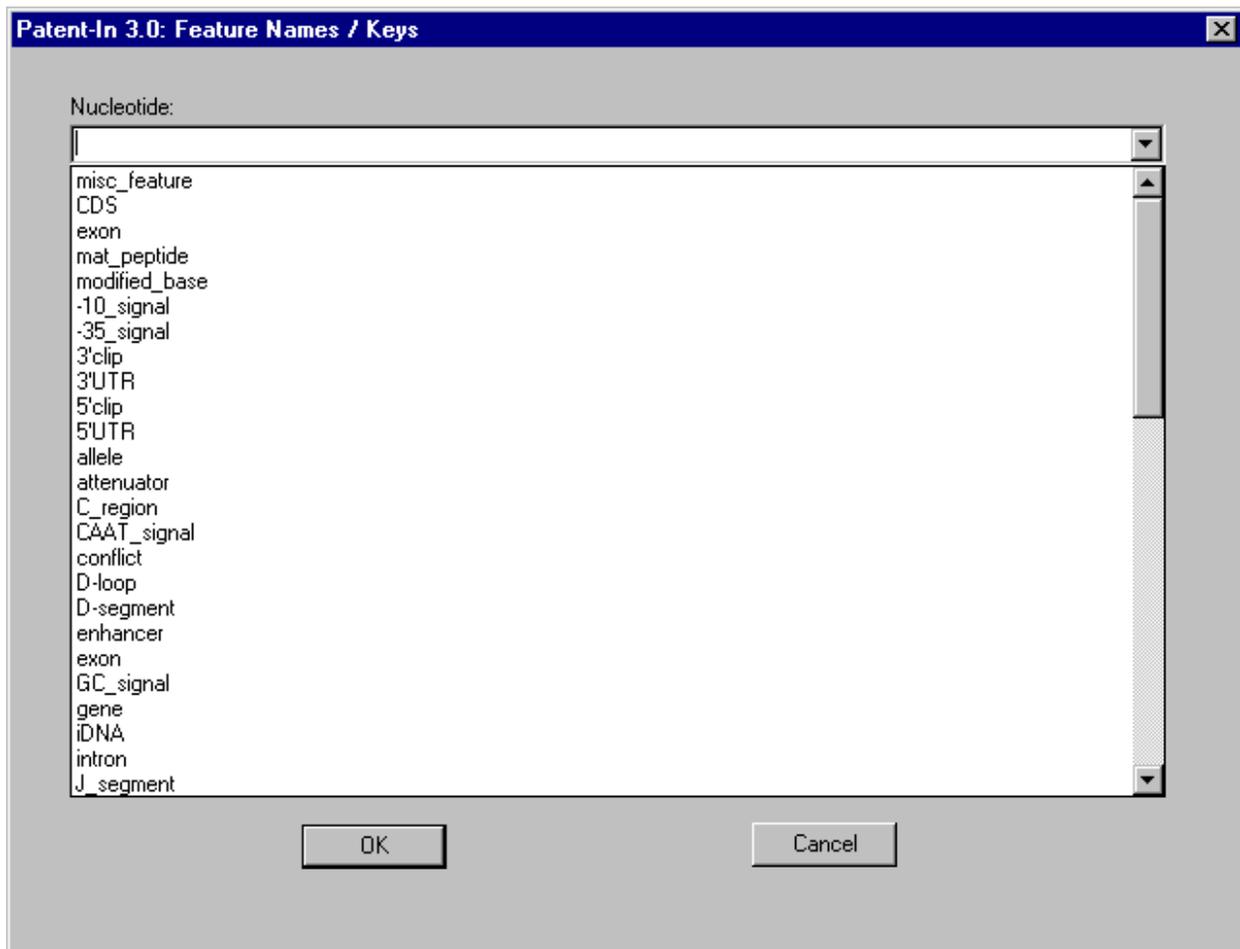


Figure 6-2: Feature Key Selection Screen

To select a Nucleotide name:

1.  Select the **Names** button on the PatentIn 3.0 Features Screen(Figure 6-1).
2.  Click on the down arrow to open the drop-down list.
3.  Click on the name.
4.  Click on **OK** to accept the selection and return to the PatentIn 3.0 Features Screen (Figure 6-1).

SECTION 7
PUBLICATION DATA

SECTION 7 PUBLICATION DATA

7.1 PATENTIN 3.0 PUBLICATION TYPE SCREEN

The PatentIn 3.0 Publication Type Screen (Figure 7-1) provides access to four screens for entering publication information. They are Journal, Database, Patent, and Thesis. You can access this screen by selecting Publication Data from the Application Steps menu.

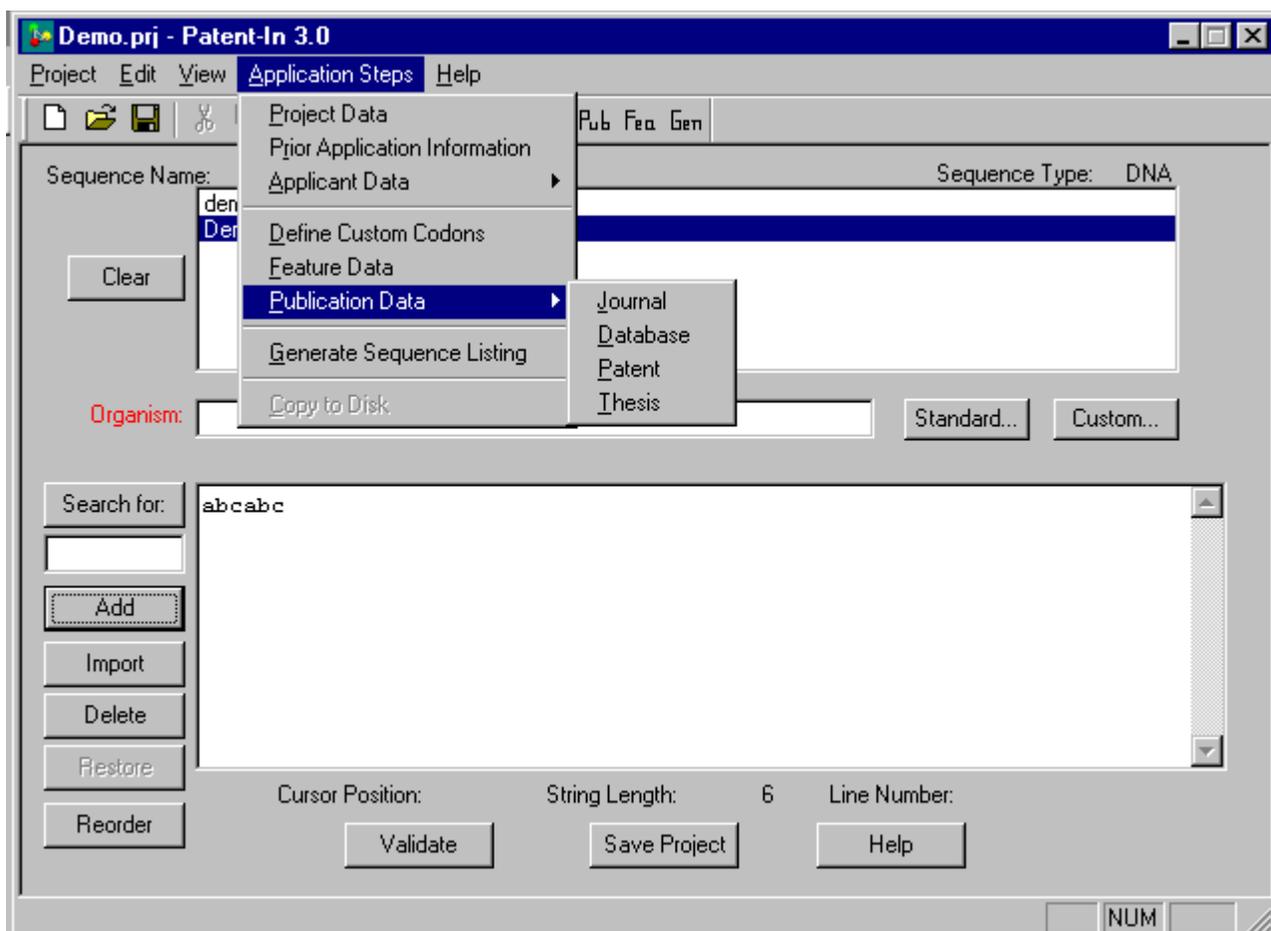


Figure 7-1: PatentIn 3.0 Publication Type Screen

To select a Publications Type:

1. From the pull down menu, **Application Steps**,  Click on **Publication Data**.

7.2 PATENTIN 3.0 JOURNAL PUBLICATION INFORMATION

The PatentIn 3.0 Journal Publication Information Screen (Figure 7-2) provides the user with a means to input published supporting scientific literature with the patent application.

The screenshot shows a software window titled "Patent-In 3.0: Journals - demo". At the top, it displays "Sequence Type: DNA" and "Sequence String Length: 0". Below this is a section for "Journal Publications" with several input fields: "Database Name / Accession Number", "Database Entry Date", "Author(s)", "Publication Title", "Journal" (a drop-down menu), "Volume", "Issue", "Publication Date", "Page Ranges", and "Relevant Residues From" to "To". A "Clear" button is located next to the "Author(s)" field. Below the input fields is a "Journal List" table with columns for "Item", "Publication Title", "Accession No.", "From", and "To". To the left of the table are buttons for "Insert", "Replace", "Delete", and "To Databases-->". At the bottom of the window are buttons for "Validate", "Save Project", "OK", "Cancel", and "Help".

Figure 7-2: PatentIn 3.0 Journal Publication Information Screen

To enter information about a Journal Publication:

1. From the Application Steps menu, select **Publication Data**, select **Journal**.
2. Enter the **Database Name / Accession Number**.
3. Enter the **Database Entry Date**.
4. Enter the name of the **Author(s)**.
5. Enter the **Publication Title**.
6. Select the **Journal** name from the drop-down pick list. If the name is not on the list you may enter it.
7. Enter the **Volume**.
8. Enter the **Issue**.

9.  Enter the **Publication Date**.
10.  Enter the **Page Ranges**.
11. In the  Enter the “**Relevant Residue From**” and “**To**” sequence position numbers.
12.  Click on the Clear button to clear the **Journal Publications** portion of the screen.
13. To insert an entry from the **Journal List**, highlight it and  click on the **Insert** button.
14. To replace an entry from the **Journal List**, highlight it and  click on the **Remove** button.
15. To delete an entry from the **Journal List**, highlight it and  click on the **Delete** button.
16. To validate the information entered,  click on **Validate**. Data entered in the table (Insert) is then validated. Information in the **Journal Publications** edit area, that has not yet been inserted, is not validated.
17. To save the information,  click on the **Save Project** button.
18. To validate and close,  click on the **OK** button.
19. To proceed to the next **Publication Data, Database**,  click on the **To Databases→** button.

7.3 PATENTIN 3.0 DATABASE PUBLICATION INFORMATION

The PatentIn 3.0 Database Publication Information Screen (Figure 7-3) provides the user with a means to input published supporting scientific database with the patent application.

Patent-In 3.0: Databases - demo

Sequence Type: DNA Sequence String Length: 0

Databases

Database Name / Accession Number: Database Entry Date:

Relevant Residues From: To:

Clear

Database List:

Item	Accession No.	From	To
------	---------------	------	----

Insert

Replace

Delete

<--To Journals

To Patents-->

Validate Save Project OK Cancel Help

Figure 7-3: PatentIn 3.0 Database Publication Information Screen

To enter information about a Database Publication:

1. From the **Application Steps** select **Publications Data**, then select **Database**.
2. Enter the **Database Name / Accession Number**.
3. Enter the **Database Entry Date**.
4. Enter the “**Relevant Residues From**” and “**To**” sequence position numbers.
5. Click on the **Clear** button to clear the **Databases** part of the screen.
6. To insert an entry into the **Patent List**, highlight it and click on the **Insert** button.
7. To replace an entry from the **Patent List**, highlight it and click on the **Remove** button.
8. To delete an entry from the **Patent List**, highlight it and click on the **Delete** button.
9. To validate the information entered, click on **Validate**. Data entered in the table (Insert) is then validated. Information in the edit area, that has not yet been inserted, is not validated.

10. To save the information, click on the **Save Project** button.
11. To validate and close, click on the **OK** button.
12. To go back to the previous **Publication Data, Journal**, click on the **← To Journals** button.
13. To proceed to the next **Publication Data, Patent**, click on the **To Patents→** button.

7.4 PATENTIN 3.0 PATENT PUBLICATIONS INFORMATION

The PatentIn 3.0 Patent Publication Information Screen (Figure 7-4) provides the user with a means to input published supporting patent publication information with the patent application.

Figure 7-4: PatentIn 3.0 Patent Publication Information Screen

To enter information about a Patent Publication:

1. From the **Application Steps** select **Publications Data**, then select **Patent**.
2. Enter the **Database Name / Accession Number**.
3. Enter the **Database Entry Date**.
4. Enter the **Document Number**.
5. Enter the **Filing Date**.
6. Enter the **Publication Date**.

7.  Enter the **Title**.
8.  Enter the “**Relevant Resides From**” and “**To**” sequence position numbers.
9.  Click on the **Clear** button to clear the **Patents** portion of the screen.
10. To insert an entry into the **Patent List**, highlight it and  click on the **Insert** button.
11. To replace an entry from the **Patent List**, highlight it and  click on the **Replace** button.
12. To delete an entry from the **Patent List**, highlight it and  click on the **Delete** button.
13. To validate the information entered,  click on **Validate**. Data entered in the table (Insert) is then validated. Information in the edit area, that has not yet been inserted, is not validated.
14. To save the information,  click on the **Save Project** button.
15. To validate and close,  click on the **OK** button.
16. To go back to the previous **Publication Data, Database**,  click on the **← To Databases** button.
17. To proceed to the next **Publication Data, Thesis**,  click on the **To Theses→** button.

7.5 PATENTIN 3.0 THESIS PUBLICATION INFORMATION

The PatentIn 3.0 Thesis Publications Information Screen (Figure 7-5) provides the user with a means to input published supporting thesis publication information with the patent application.

Patent-In 3.0: Thesis

Sequence Name: DNA Sequence String Length: 6

Theses

Database Name / Accession Number: Database Entry Date:

Author(s):

Clear Title:

Publication Date: Page Ranges:

Relevant Residues From: To:

Thesis List:

Item	Title	Accession No.	From	To
------	-------	---------------	------	----

Insert

Replace

Delete

<--To Patents

Validate Save Project OK Cancel Help

Figure 7-5: PatentIn 3.0 Thesis Publications Information Screen

To enter information about a Thesis Publication:

1. From the **Application Steps** select **Publications Data**, select **Thesis**.
2. Enter the **Database Name / Accession Number**.
3. Enter the **Database Entry Date**.
4. Enter the **Author Name**.
5. Enter the **Title**.
6. Enter the **Publication Date**.
7. Enter the **Page Ranges**.
8. Enter the **“Relevant Residues From”** and **“To”** sequence position numbers.
9. Click on the **Clear** button to clear the **Theses** portion of the screen.
10. To insert an entry into the **Thesis List**, highlight it and click on the **Insert** button.
11. To replace an entry from the **Thesis List**, highlight it and click on the **Replace** button.

12. To delete an entry from the **Thesis List**, highlight it and  click on the **Delete** button.
13. To validate the information entered,  click on **Validate**. Data entered in the table (Insert) is then validated. Information in the edit area, that has not yet been inserted, is not validated.
14. To save the information,  click on the **Save Project** button.
15. To validate and close,  click on the **OK** button.
16. To go back to the previous **Publication Data, Patent**,  click on the **←To Patents** button.

 NOTE: FOR THE PUBLICATION DATA, VALIDATION IS DONE ON ALL OF THE INSERTED DATA.

SECTION 8
CREATING A SEQUENCE LISTING PROJECT FILE

SECTION 8 CREATING A SEQUENCE LISTING FILE

8.1 SEQUENCE LISTING FILE

The sequence listing file includes all the information required by the ST.25 standard. PatentIn 3.0 generates a sequence listing file names “ST25.txt, and places it in the directory containing the project.

8.2 GENERATING A SEQUENCE LISTING FILE

The PatentIn 3.0 Sequence Generation Screen (Figure 8-1) notifies the user that the Generate process is about to occur and gives the option to be notified if any errors occur during the process.

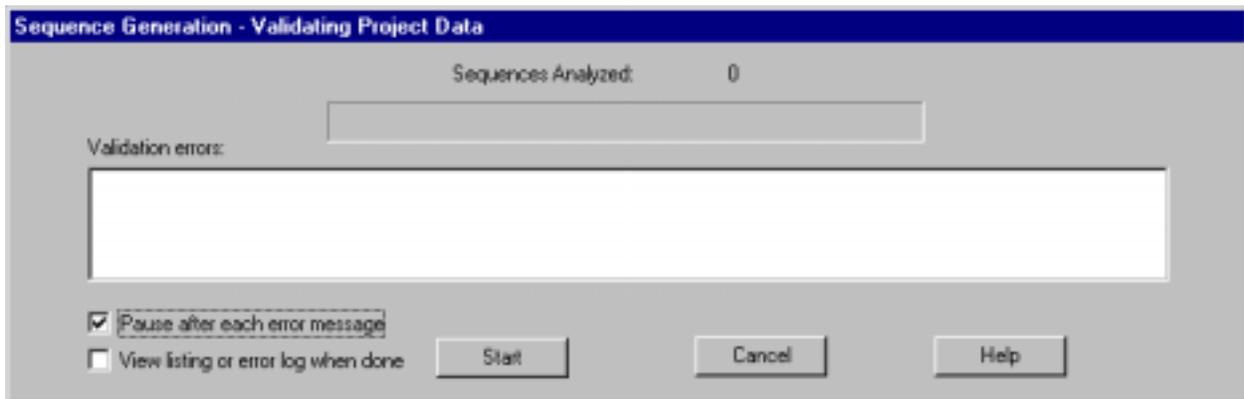


Figure 8-1: PatentIn 3.0 Sequence Generation Screen

To Generate a Sequence Listing:

1.  Select **Generate Sequence Listing** from the **Application Steps** menu (Figure 4-1).
2.  Click in the box next to “Pause after each error message” if you wish to be notified of an error in the sequence data.
3.  Click on the **Start** the sequence generation.

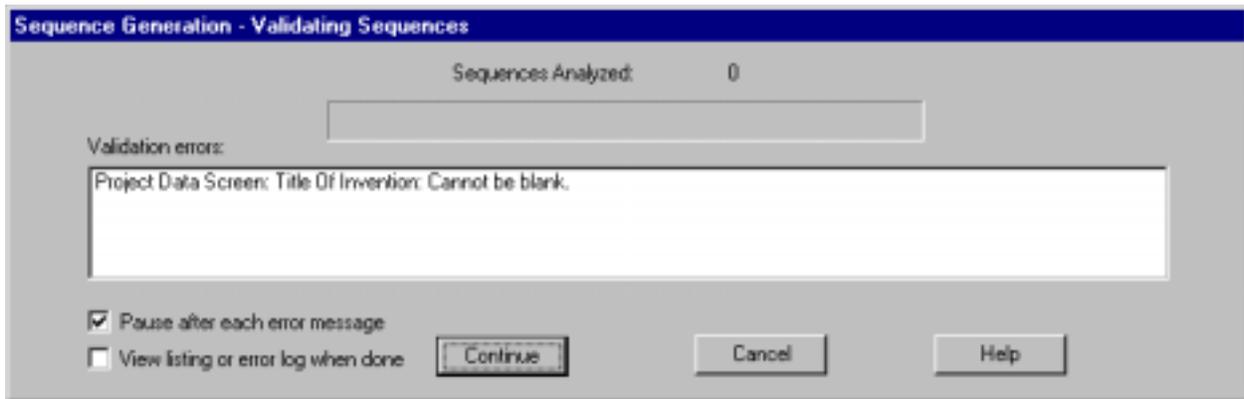


Figure 8-2: Second Sequence Generation Screen

4.  Click on the Continue button to continue validation.
5.  Click on the Cancel button to cancel validation.
6. If an error message is displayed and Pause was selected, an error message will appear and validation will pause.

8.3 VIEWING A SEQUENCE LISTING FILE

To view a Sequence Listing Project File:

1. If sequence generation succeeded and **View listing or error log when done** was selected, the sequence listing will be shown automatically. If **View listing or error log when done** was not selected you can view the sequence by selecting **View Sequence Listing** from the **Project** menu.

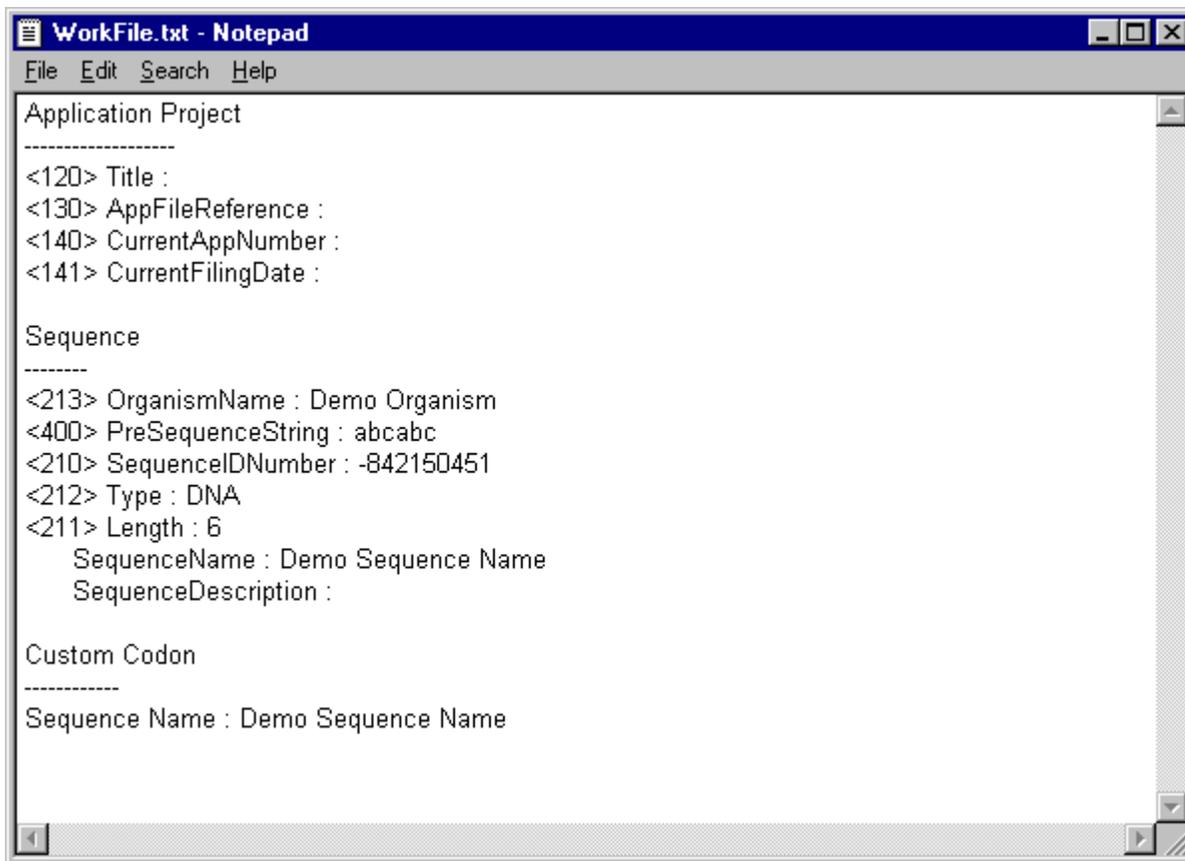


Figure 8-3: View Results Window

i SPECIAL NOTE FOR USERS WITH VERY LARGE SEQUENCES AND LARGE NUMBERS OF SEQUENCES: PTO has located a viewer that really works for very large text files. A 60 day evaluation version is downloadable at www.fileviewer.com <<http://www.fileviewer.com>> . The viewer is named "V" and version 2000 SR-1. It was tested with 60MB and 120MB files and "worked great." It should manage files of almost any size. It was tested on a laptop with Win98. (LocalAdmin may be required for installation.)

8.4 COPYING THE SEQUENCE LISTING TO A DISK

The PatentIn 3.0 Copy to Disk Screen (Figure 8-4) provides the user with the means to name: the drive name to where the file is to be copied, the filename for the copied file and the type of the copied file.

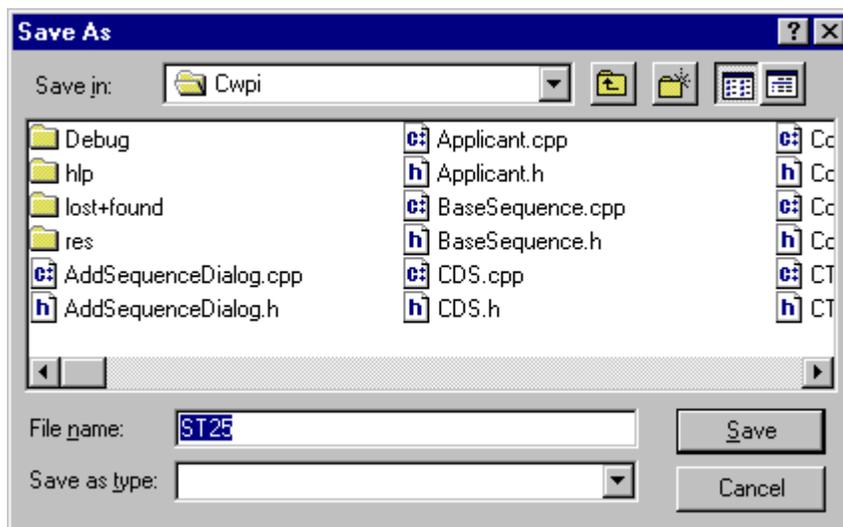


Figure 8-4: PatentIn 3.0 Copy to Disk Screen

To copy a sequence listing:

1.  Select **C**opy to Disk from the **A**pplication Steps menu (Figure 4-1).
2.  Enter the drive name (Figure 8-4) in the **S**ave in field.
3.  Enter the File name in the **F**ile name field.
4.  Select the type **.txt** or **.zip** in the **S**ave in: field.
5.  Click on **S**ave to submit the application.

If **.txt** is selected, PatentIn checks to see if there is enough free disk space to receive the listing file. If so, the file will be copied to the selected location. If not, PatentIn will suggest **.zip**.

 **NOTE: .ZIP WORKS ONLY WITH FLOPPY DISK AND WILL FORMAT THE DISK BEFORE WRITING ANYTHING TO THE DISK.**

APPENDIX A
LIST OF ACRONYMS

APPENDIX A LIST OF ACRONYMS

MB	Megabytes
MHz	Megahertz
PC	Personal Computer
URL	Universal Resource Locator
USPTO	United States Patent and Trademark Office
WIPO	World Intellectual Property Organization
WPI	Web PatentIn
WWW	World Wide Web

APPENDIX B
FIELD IDENTIFIERS, LENGTHS AND TYPES

APPENDIX B FIELD IDENTIFIERS, LENGTHS AND TYPES

Table B-1, below, includes a complete list of all field names that appear in the data entry screens, and corresponding field identifiers, field lengths, and field types. Field identifiers are used to separate WPI data into raw data files, and Sequence Listing Project Files.

Table B-1: Field Name, Identifier, Size, and Type

Field Identifier	Field Name	Field Length	Field Type A-alpha N- numeric
N/A	Project Name	8	AN
<110>	Applicant Name	1200	AN
<120>	Title of Invention	240	AN
<130>	File Reference	60	AN
<140>	Current Application Number	23	AN
<141>	Current Filing Date	8	N
<150>	Earlier Application Number	23	AN
<151>	Earlier Filing Date	8	N
N/A	Sequence File Name	8	AN
<160>	Number of Sequences	5	N
<170>	Software	60	AN
<210>	Information for SEQ ID No.	5	N
<211>	Length	6	N
<212>	Type	3	A
<213>	Organism	60	AN
<220>	Feature	0	B
<221>	Name/key	20	AN
<222>	Location	12	N
<223>	Other Information	260	AN
<300>	Publication Information	0	B
<301>	Authors	120	AN
<302>	Title (of Publication)	120	AN
<303>	Journal (name)	40	AN

<304>	Volume	5	AN
<305>	Issue	5	AN
<306>	Pages	20	AN
<307>	Date	30	AN
<308>	Database Accession Number	45	AN
<309>	Database Entry Date	8	N
<310>	Document number	18	AN
<311>	Filing Date	8	N
<312>	Publication Date	8	N
<313>	Relevant Residues	20	N
<400>	Sequence Description	100,000	AN

APPENDIX C
COUNTRY CODES

APPENDIX C COUNTRY CODES

Table C-1 includes a complete list of country codes that are used when completing the **Current Application Number** field in the **PatentIn 3.0 Project Data Screen** (Figure 4-2) and the **Prior Application Number** field in the **PatentIn 3.0 Prior Application Information Screen**(Figure 4-3).

Table C-1: Country Codes

Code	Country
AF	Afghanistan
OA	African Intellectual Property Organization (OAPI)
AP	African Regional Industrial Property Organization (ARIPO)
AL	Albania
DZ	Algeria
AO	Angola
AI	Anguilla
AG	Antigua & Barbuda
AR	Argentina
AU	Australia
AT	Austria
BS	Bahamas
BH	Bahrain
BD	Bangladesh
BB	Barbados
BE	Belgium
BZ	Belize
BX	Benelux Trademark Office and Benelux Designs Office
BJ	Benin
BM	Bermuda
BT	Bhutan
BO	Bolivia

Code	Country
BW	Botswana
BR	Brazil
VG	British Virgin Islands
BN	Brunei Darussalam
BG	Bulgaria
BF	Burkina Faso
BU	Burma
BI	Burundi
CM	Cameroon
CA	Canada
CV	Cape Verde
KY	Cayman Islands
CF	Central African Republic
TD	Chad
CL	Chile
CN	China
CO	Columbia
KM	Comoros
CG	Congo
CR	Costa Rica
CI	Cote d'Ivoire
CU	Cuba
CY	Cyprus
CS	Czechoslovakia
KH	Democratic Kampuchea
KP	Democratic People's Republic of Korea
YD	Democratic Yemen
DK	Denmark
DJ	Djibouti

Code	Country
DM	Dominica
DO	Dominican Republic
EC	Ecuador
EG	Egypt
SV	El Salvador
GQ	Equatorial Guinea
ET	Ethiopia
EP	European Patent Office (EPO)
FK	Falkland Islands (Malvinas)
FJ	Fiji
FI	Finland
FR	France
GA	Gabon
GM	Gambia
DD	German Democratic Republic
DE	Germany, Federal Republic of
GH	Ghana
GI	Gibraltar
GR	Greece
GD	Grenada
GT	Guatemala
GN	Guinea
GW	Guinea-Bissau
GY	Guyana
HT	Haiti
VA	Holy See
HN	Honduras
HK	Hong Kong
HU	Hungary

Code	Country
IS	Iceland
IN	India
ID	Indonesia
IR	Iran (Islamic Republic of)
IQ	Iraq
IE	Ireland
IL	Israel
IT	Italy
JM	Jamaica
JP	Japan
JO	Jordan
KE	Kenya
KI	Kiribati
KW	Kuwait
LA	Laos
LB	Lebanon
LS	Lesotho
LR	Liberia
LY	Libya
LI	Liechtenstein
LU	Luxembourg
MG	Madagascar
MW	Malawi
MY	Malaysia
MV	Maldives
ML	Mali
MT	Malta
MR	Mauritania
MU	Mauritius

Code	Country
MX	Mexico
MC	Monaco
MN	Mongolia
MS	Montserrat
MA	Morocco
MZ	Mozambique
NR	Nauru
NP	Nepal
NL	Netherlands
AN	Netherlands Antilles
NZ	New Zealand
NI	Nicaragua
NE	Niger
NG	Nigeria
NO	Norway
OM	Oman
PK	Pakistan
PA	Panama
PG	Papua New Guinea
PY	Paraguay
PE	Peru
PH	Philippines
PL	Poland
PT	Portugal
QA	Qatar
KR	Republic of Korea
RO	Romania
RW	Rwanda
KN	Saint Christopher & Nevis

Code	Country
SH	Saint Helena
LC	Saint Lucia
VC	Saint Vincent & the Grenadines
WS	Samoa
SM	San Marino
ST	Sao Tome & Principe
SA	Saudi Arabia
SN	Senegal
SC	Seychelles
SL	Sierra Leone
SG	Singapore
SB	Solomon Islands
SO	Somalia
ZA	South Africa
SU	Soviet Union
ES	Spain
LK	Sri Lanka
SD	Sudan
SR	Suriname
SZ	Swaziland
SE	Sweden
CH	Switzerland
SY	Syria
TW	Taiwan, Province of China
TH	Thailand
TG	Togo
TO	Tonga
TT	Trinidad & Tobago
TN	Tunisia

Code	Country
TR	Turkey
TV	Tuvalu
UG	Uganda
AE	United Arab Emirates
GB	United Kingdom
TZ	United Republic of Tanzania
US	United States of America
UY	Uruguay
VU	Vanuatu
VE	Venezuela
VN	Viet Nam
WO	World Intellectual Property Organization (WIPO)
YE	Yemen
YU	Yugoslavia
ZR	Zaire
ZM	Zambia
ZW	Zimbabwe

APPENDIX D
TABLE TO EXCHANGE NUCLEOTIDE CHARACTERS AND AMINO
CHARACTERS

APPENDIX D
TABLE TO EXCHANGE NUCLEOTIDE CHARACTERS AND AMINO CHARACTERS

Table D-1 provides a list of acceptable characters to be used for hand keying PRT/1 data into the sequence description field, importing PRT/3 data, and converting PRT/1 data in the sequence description field. The nucleotide equivalent data is utilized during sequence listing project file generation when all CDS featured codons (three letter nucleotides) are translated into an amino abbreviated name (PRT/3).

Table D-1: Exchange Nucleotide Characters and Amino Characters

PRT/1	PRT/3	Nucleotide Equivalent
A	Ala	gcu, gcc, gca, gcg, gct
R	Arg	cgu, cgc, cga, cgg, cgt, aga, agg
N	Asn	aau, aac, aat
D	Asp	gau, gac, gat
B	Asx	
C	Cys	ugu, ugc, tgt, tgc
Q	Gln	caa, cag
E	Glu	gaa, gag
Z	Glx	
G	Gly	ggu, ggc, gga, ggg, ggt
H	His	cau, cac, cat
I	Ile	auu, auc, aua, att, atc, ata
L	Leu	uua, uug, cuu, cuc, cua, cug, tta, ttg, ctt, ctc, cta, ctg
K	Lys	aaa, aag
M	Met	aug, atg
F	Phe	uuu, ucc, ttt, ttc
P	Pro	ccu, ccc, cca, ccg, cct
S	Ser	ucu, ucc, uca, ucg, tct, tcc, tca, tcg, agu, agc, agt
T	Thr	acu, acc, aca, acg, act

PRT/1	PRT/3	Nucleotide Equivalent
W	Trp	ugg, tgg
Y	Tyr	uau, uac, tat, tac
V	Val	guu, guc, gua, gug, gtt, gtc, gta, gtg
X	Xaa	any set containing "n"

APPENDIX E
NUCLEOTIDE SEQUENCE FEATURES

APPENDIX E NUCLEOTIDE SEQUENCE FEATURES

Table E-1 provides a list (in alphanumeric order) of **Nucleotide** sequence features that are displayed in the PatentIn 3.0 Features Screen when you have previously selected DNA or RNA as the **Sequence Type** and  clicked on the **Names** button. A list of nucleotides appears in a pick list after  clicking on the down arrow at the end of the **Nucleotide** box. After  clicking on a sequence feature in the pick list, the sequence feature name appears in the **Feature Name / Key** field (<221>).

Table E-1: Nucleotide Sequence Features

Nucleotide Sequence Features
-10_signal
3'clip
3'UTR
-35_signal
5'clip
5'UTR
Allele
Attenuator
C_region
CAAT_signal
CDS
Conflict
D-loop
D-segment
Enhancer
Exon
GC_signal
Gene
IDNA
Intron
J_segment

Nucleotide Sequence Features
LTR
Mat_peptide
misc_binding
misc_difference
misc_feature
misc_recomb
misc_RNA
misc_signal
misc_structure
Modified_base
MRNA
Mutation
N_region
old_sequence
polyA_signal
polyA_site
precursor_RNA
prim_transcript
primer_bind
Promoter
protein_bind
RBS
rep_origin
repeat_region
repeat_unit
RRNA
S_region
Satellite
ScRNA

Nucleotide Sequence Features
sig_peptide
SnRNA
Source
stem_loop
STS
TATA_signal
Terminator
transit_peptide
TRNA
Unsure
V_region
V_segment
Variation

APPENDIX F
AMINO ACID SEQUENCE FEATURES

APPENDIX F

AMINO ACID SEQUENCE FEATURES

Table F-1 provides a list (in alphabetical order) of **AminoAcids** sequence features that are displayed in the PatentIn 3.0 Features Screen when you have previously selected PRT as the **Sequence Type** and  clicked on the **Names** button. The listed sequence features appear in a pick list after  clicking on the down arrow at the end of the **AminoAcids** box. After  clicking on a sequence feature in the pick list, the sequence feature name appears in the **Feature Name / Key** field.

Table F-1: Amino Acid Sequence Features

Amino Acid Sequence Features
ACT_SITE
BINDING
CA_BIND
CARBOHYD
CHAIN
CONFLICT
DISULID
DNA_BIND
DOMAIN
HELIX
INIT_MET
LIPID
METAL
MOD_RES
MUTAGEN
NON_CONS
NON_TER
NP_BIND
PEPTIDE
PROPEP
REPEAT
SIGNAL

Amino Acid Sequence Features
SIMILAR
SITE
STRAND
THIOETH
THIOLEST
TRANSIT
TRANSMEM
TURN
UNSURE
VARIANT
VARSP LIC
ZN_FING

APPENDIX G
DATA TABLES FOR MOD_RES SEQUENCE FEATURES

APPENDIX G

DATA TABLES FOR MOD_RES SEQUENCE FEATURES

Appendix G provides a list (in alphabetical order) of additional modified residue (MOD_RES) **Sequence Features** that are displayed in the PatentIn 3.0 Features Screen when you have previously selected PRT as the **Sequence Type**, and MOD_RES from the listed sequence features in the pick list. After clicking on a sequence feature in the pick list, **MOD_RES** appears in the **Feature Name / Key** field (<221>), and the first **Add the following MOD-RES to the Other Information** field for MOD_RES (Table G-1) and second **Add the following MOD-RES to the Other Information** field for MOD_RES (Table G-2) sequence features appears. You can select from either one or both of the **Add the following MOD-RES to the Other Information** fields, and the data will appear in the **Other Information** field (<223>).

Table G-1: First Data Table for MOD_RES Sequence Features

First Data Table for MOD_RES Sequence Features
Blank space (default option)
ACETYLATION
AMIDATION
BLOCKED
FORMYLATION
GAMMA-CARBOXYGLUTAMIC ACID HYDROXYLATION
METHYLATION
PHOSPHORYLATION
PYRROLIDONE CARBOXYLIC ACID
SULFATATION

Table G-2: Second Data Table for MOD_RES Sequence Features

Second Data Table for MOD_RES Sequence Features	
Symbol	Meaning
	Blank space (default option)
Aad	2-Amino adipic acid
Baad	3-Amino adipic acid
Bala	beta-Alanine, beta-Aminopropionic acid
Abu	2-Aminobutyric acid

Second Data Table for MOD_RES Sequence Features	
Symbol	Meaning
4Abu	4-Aminobutyric acid, piperidinic acid
Acp	6-Aminocaproic acid
Ahe	2-Aminoheptanoic acid
Aib	2-Aminoisobutyric acid
BAib	3-Aminoisobutyric acid
Apm	2-Aminopimelic acid
Dbu	2,4 Diaminobutyric acid
Des	Desmosine
Dpm	2,2'-Diaminopimelic acid
Dpr	2,3-Diaminopropionic acid
EtGly	N-Ethylglycine
EtAsn	N-Ethylasparagine
Hyl	Hydroxylysine
AHyl	allo-Hydroxylysine
3Hyp	3-Hydroxyproline
4Hyp	4-Hydroxyproline
Ide	Isodesmosine
Alle	allo-Isoleucine
MeGly	N-Methylglycine, sarcosine
Melle	N-Methylisoleucine
MeLys	6-N-Methyllysine
MeVal	N-Methylvaline
Nle	Norleucine
Nva	Norvaline
Orn	Ornithine

APPENDIX H
ADDITIONAL LIPID SEQUENCE FEATURES

APPENDIX H ADDITIONAL LIPID SEQUENCE FEATURES

Table H-1 provides a list (in alphabetical order) of additional lipid sequence features that are displayed in the PatentIn 3.0 Features Screen when you have previously selected PRT as the **Sequence Type**, and **LIPID** from the listed sequence features in the pick list. After clicking on a **Sequence Feature** in the **Sequence Feature Pick List**, lipid appears in the **Feature Name / Key** field (<221>) and the **Add the following LIPID to the Other Information field** appears. When you select from the **Add the following LIPID to the Other Information field**, the data appears in the **Other Information** field (<223>).

Table H-1: Additional Lipid Sequence Features

Additional Lipid Sequence Features
FRAMESYL
GERANYL-GERANYL
GPI-ANCHOR
MYRISTATE
N-ACYL DIGLYCERIDE
PALMITATE

APPENDIX I
ACCEPTABLE CHARACTERS IN THE SEQUENCE DESCRIPTION
FIELD

APPENDIX I

ACCEPTABLE CHARACTERS IN THE SEQUENCE DESCRIPTION FIELD

Table I-1 provides an acceptable list of characters used as a filter for hand keying or importing DNA or RNA data into the sequence description field. PRT/1 and PRT/3 data lists are used during sequence listing project file generation when all single letter protein data is translated into amino abbreviated name (PRT/3) data.

Table I-1: Acceptable Characters in the Sequence Description Field

DNA	RNA	DNA/RNA	Protein/1	Protein/3
A	A	A	A	Ala
G	G	G	C	Cys
C	C	C	D	Asp
T		T	E	Glu
	U	U	F	Phe
R	R	R	G	Gly
Y	Y	Y	H	His
M	M	M	I	Ile
K	K	K	K	Lys
S	S	S	L	Leu
W	W	W	M	Met
B	B	B	N	Asn
D	D	D	P	Pro
H	H	H	Q	Gln
V	V	V	R	Arg
N	N	N	S	Ser
			T	Thr
			V	Val
			W	Trp
			Y	Tyr
			B	Asx
			Z	Glx
			X	Xaa

APPENDIX J
ADDITIONAL MODIFIED_BASE SEQUENCE FEATURES

APPENDIX J

ADDITIONAL MODIFIED_BASE SEQUENCE FEATURES

Table J-1 provides a list (in alphabetical order) of additional **modified_base** sequence features that are displayed in the PatentIn 3.0 Features Screen when you have previously selected DNA or RNA as the **Sequence Type**, and **modified_base** from the listed sequence features in the pick list. After clicking on a sequence feature in the list, **modified_base** appears in the **Feature Name / Key** field (<221>), and the **Add the following Modified_base to the Other Information** field appears in the PatentIn 3.0 Features Screen. The user selects from the pick lists, and the data appears in the **Other Information** field (<223>).

Table J-1: Modified_base Sequence Features

Symbol	Meaning
ac4c	4-acetylcytidine
chm5u	5-(carboxyhydroxymethyl)uridine
cm	2'-o-methylcytidine
cmnm5s2u	5-carboxymethylaminomethyl-2-thiouridine
cmnm5u	5-carboxymethylaminomethyluridine
d	dihydrouridine
fm	2'-O-methylpseudouridine
gal q	Beta, D-galactosylquesosine
gm	2'-O-methylguanosine
i	inosine
i6a	N6-isopentenyladenosine
m1a	1-methyladenosine
m1f	1-methylpseudouridine
m1g	1-methylguanosine
m1i	1-methylinosine
m22g	2,2,-dimethylguanosine
m2a	2-methyladenosine
m2g	2-methylguanosine
m3c	3-methylcytidine
m5c	5-methylcytidine

Symbol	Meaning
m6a	N6-methyladenosine
m7g	7-methylguanosine
mam5u	5-methylaminothyluridine
mam5s2u	5-methyloxyaminomethyl-2-thiouridine
man q	beta, D-mannosylqueosine
mcm5s2u	5-methyloxycarbonylmethyl-2-thiouridine
mcm5u	5-methyloxycarbonylmethyluridine
mo5u	5-methyloxyuridine
ms2i6a	2-methylthio-N6-isopentenyladenosine
ms2t6a	N-((9-beta-D-ribofuranosyl-2-methylthiopurine-6-yl) carbamoyl)threonine
mt6a	N-((9-beta-D-ribofuranosylpurine-6-yl)-methylcarbamoyl)threonine
mv	uridine-5-oxyacetic acid-methylester
o5u	uridine-5-oxyacetic acid (v)
osyw	wybutoxosine
p	pseudouridine
q	queosine
s2c	2-thiocytidine
s2t	5-methyl-2-thiouridine
s2u	2-thiouridine
s4u	4-thiouridine
t	5-methyluridine
t6a	N-((9-beta-D-ribofuranosylpurine-6-yl)-carbamoyl)threonine
Tm	2'-O-methyl-5-methyluridine
Um	2'-O-methyluridine
Yw	wybutosine
X	3-(3-amino-3-carboxy-propyl)uridine, (acp3)u