

Configuring Dialog Settings

In the dialog you can setup the corresponding parameters:

Window size — the number of bases in a window. The window size should be greater than 2. The default value is 100 bp.

Window step — the number of bases used to shift a window. The *Window step* should be a positive integer. The default value is 1 bp.

Threshold — the threshold value of the twist angle (see above). The default value is 13.7.

You can remember the input values or restore the default values using the *Remember Setting* and the *Restore Defaults* buttons.

The annotations names and other parameters can be changed on the *Output* tab of the dialog:

The screenshot shows the 'DNA Flexibility' dialog box with the 'Output' tab selected. The dialog has a title bar with a 'U' icon and the text 'DNA Flexibility'. Below the title bar are two tabs: 'Search Settings' and 'Output'. The 'Output' tab contains the following settings:

- Save annotation(s) to:**
 - ☒ Existing table: A dropdown menu showing 'NC_001363 features [murine.gb]' with a file icon button to its right.
 - ☐ Create new table: An empty text input field with a three-dot menu button to its right.
 - ☐ Use auto-annotations table
- Annotation parameters:**
 - Group name:** A text input field containing '<auto>' with a snowflake icon button to its right.
 - Annotation name:** A text input field containing 'dna_flex'.
 - Description:** An empty text input field.

At the bottom of the dialog are three buttons: 'Search' (highlighted in blue), 'Cancel', and 'Help'.

Once the *Search* button has been pressed, the [annotations](#) for the regions of the high DNA flexibility are created.