

Tandem Repeats Finding

To find tandem repeats, select the *Analyze Find tandems...* context menu item in the *Sequence View* window.

In the opened dialog you can specify the tandem search parameters, the region to search in and the result parameters:

The 'Find Tandems' dialog box is shown with the 'Base' tab selected. It contains the following fields and controls:

- Tandem finder parameters:**
 - Tandem preset:** A dropdown menu set to 'Custom'.
 - Min period:** A text box containing '31 n' with up/down arrow buttons.
 - Max period:** A text box containing '1000000 n' with up/down arrow buttons.
- Region to process:**
 - Region:** A dropdown menu set to 'Whole sequence'.
 - Start/End:** Two text boxes containing '1' and '199950' respectively, separated by a hyphen.
- Save annotation(s) to:**
 - ☐ Existing table: A dropdown menu.
 - ☒ Create new table: A text box.
- Annotation parameters:**
 - Group name:** A text box containing '<auto>'.
 - Annotation name:** A text box containing 'repeat_unit'.

At the bottom are three buttons: 'Start', 'Cancel', and 'Help'.

The dialog parameters:

Tandem preset — specify the tandem repeats parameters with predefined values by selecting the available preset:

This screenshot shows the 'Find Tandems' dialog box with the 'Tandem preset' dropdown menu open. The menu lists the following options:

- Custom
- All
- Micro-satellites
- Mini-satellites
- Big-period tandems
- Custom

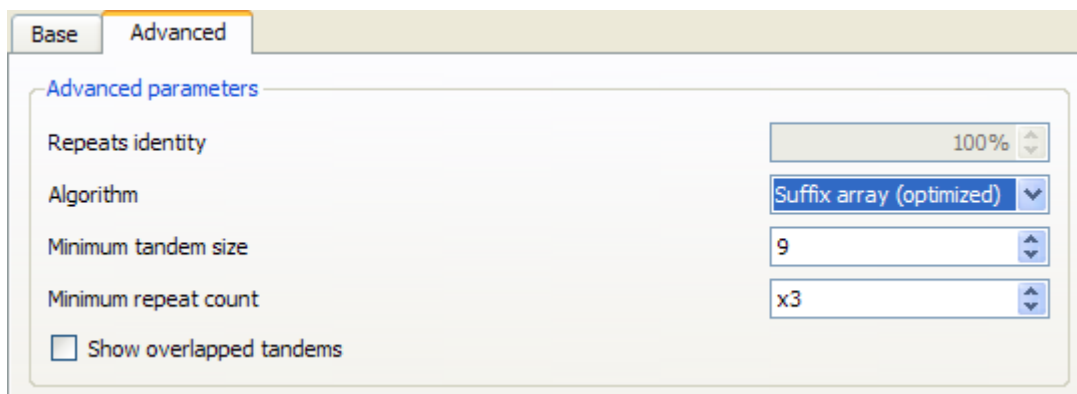
The 'Custom' option at the bottom of the list is highlighted. The other fields in the dialog remain the same as in the previous screenshot.

Min period, Max period — the minimum and maximum acceptable repeat length measured in base symbols.

Region to process — specify the region to search in the whole sequence, a custom region or the region of the current selection (if any).

Save annotation(s) to — specify the existing or new annotations table file to save the resulting annotations into.

Annotation parameters — you can change the default group name and annotation(s) name values of the resulting annotation(s).



The screenshot shows a software window with two tabs: 'Base' and 'Advanced'. The 'Advanced' tab is selected. Below the tabs, there is a section titled 'Advanced parameters' in blue text. This section contains five settings:

- Repeats identity**: A text box with '100%' and a small up/down arrow icon on the right.
- Algorithm**: A dropdown menu with 'Suffix array (optimized)' selected and a downward arrow icon on the right.
- Minimum tandem size**: A text box with '9' and a small up/down arrow icon on the right.
- Minimum repeat count**: A text box with 'x3' and a small up/down arrow icon on the right.
- Show overlapped tandems**: An unchecked checkbox followed by the text 'Show overlapped tandems'.

Additional search options can be found in the *Advanced* tab:

Algorithm — the algorithm parameter allows to select the search algorithm. The default and a fast one is optimized suffix array algorithm.

Minimum tandem size — the minimum tandem size sets the limit on minimum acceptable length of the tandem, i.e. the minimum total repeats length of the searched tandem.

Minimum repeat count — the minimum number of repeats of a searched tandem.

Show overlapped tandems — check if the plugin should search for the overlapped tandems, otherwise keep unchecked.

- [Tandem Repeats Search Result](#)