

# Tandem Repeats Finding

To find tandem repeats, select the *Analyze Find tandem repeats...* 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:

**Find Tandem Repeats**

**General** **Output**

**Settings**

Preset settings: All

Algorithm: Suffix array (opt)

Min length of repeated sequence: 1 n

Max length of repeated sequence: 1000000 n

Min length of tandem repeat: 9

Min number of repeats: x3

☐ Show overlapped tandems

**Search in**

Region: Whole sequence 1 - 199950

Help Cancel Start

The dialog parameters:

*Present Settings* — specify the tandem repeats parameters with predefined values by selecting the available preset.

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

*Min length of repeated sequence* - the minimum acceptable repeat length measured in base symbols.

*Max length of repeated sequence* - the maximum acceptable repeat length measured in base symbols.

*Min length of tandem repeat* - the minimum tandem size sets the limit on the minimum acceptable length of the tandem, i.e. the minimum total repeats length of the searched tandem.

*Min number of repeats* - 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.

*Search in* - specify the region to search in the whole sequence, a custom region or the region of the current selection (if any).

The output settings can be found in the *Output* tab:

In the *Save annotation(s) to group*, you can set up a file to store annotations. It could be either an existing annotation table object, a new annotation table or auto-annotations table (if it is available).

In the *Annotation parameters* group, you can specify the name of the group and the name of the annotation. If the group name is set to <auto> UGENE will use the group name as the name for the group. You can use the '/' characters in this field as a group name separator to create subgroups. If the annotation name is set to *by type* UGENE will use the annotation type from the *Annotation type:* table as the name for the annotation. Also, you can add a description in the corresponding text field.

- Tandem Repeats Search Result