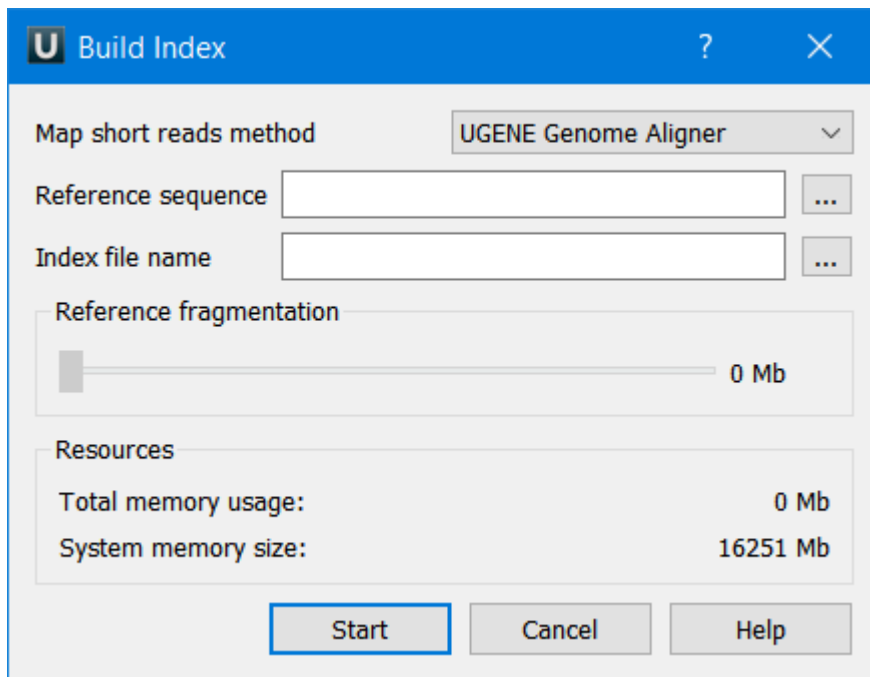


# Building Index for UGENE Genome Aligner

You can build an index to optimize short reads alignment using [UGENE Genome Aligner](#). To open the *Build Index* dialog, select the *Tools* *NGS data analysis* *Build index for reads mapping* item in the main menu. Set value of the *Map short reads method* parameter to *UGENE Genome Aligner*.

The dialog looks as follows:



The screenshot shows the 'Build Index' dialog box. The title bar is blue with a 'U' icon, a question mark, and a close button. The main area has a light gray background. The 'Map short reads method' is a dropdown menu set to 'UGENE Genome Aligner'. Below it are two text input fields: 'Reference sequence' and 'Index file name', each with a browse button ('...'). Below these is a 'Reference fragmentation' section with a slider bar and a label '0 Mb'. At the bottom is a 'Resources' section with two rows: 'Total memory usage: 0 Mb' and 'System memory size: 16251 Mb'. At the very bottom are three buttons: 'Start', 'Cancel', and 'Help'.

The parameters are the following:

*Reference sequence* — DNA sequence to which short reads would be aligned to. This parameter is required.

*Index file name* — file to save index to. This parameter is required.

*Reference fragmentation* — this parameter influences the amount of parts the reference will be divided. It is better to make it bigger, but it influences the amount of memory used during the alignment.

*Total memory usage* — shows the total memory usage.

*System memory size* — shows the total system memory size.