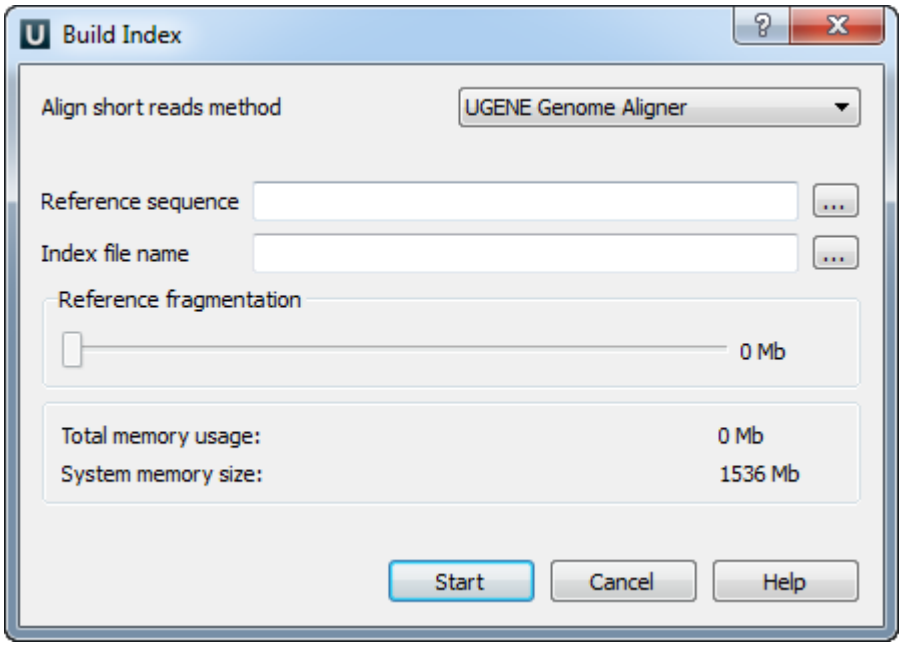
# Building Index for UGENE Genome Aligner

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 *Align short reads method* parameter to *UGENE Genome Aligner*.

The dialog looks as follows:




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 devided. 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.