## **BWA-MEM**

BWA is a fast light-weighted tool that aligns relatively short reads to a reference sequence. Click this link to open BWA homepage. BWA-MEM is generally recommended for high-quality queries as it is faster and more accurate. BWA-MEM also has better performance than BWA-backtrack for 70-100bp Illumina reads.

Open Tools Align to reference submenu of the main menu.



Select the Align short reads item to align short reads to a DNA sequence using BWA-MEM. Or select the Build index item to build an index for a DNA sequence which can be used to optimize aligning of short reads.

- Aligning Short Reads with BWA-MEMBuilding Index for BWA-MEM