

bwa-mem2

How to use:

Available versions and modules:

Version	Module
2.2.1	bioinfo/bwa-mem2

Example:

- This example can be found on the official git page ([bwa-mem2](#))
- you need to download `human_g1k_v37.fasta`

indexing.sge

```
#!/bin/bash
#$ -N bwa-mem2_indeksiranje
#$ -cwd
#$ -pe p28-mpisingle 2
#$ -l memory=40

module load bioinfo/bwa-mem2/2.2.1

bwa-mem2 index human_g1k_v37.fasta
```



In case of large input data

For indexing you need large amount of RAM memory. It is roughly 28 GB of RAM per GB of data. You need to use `-l` memory parameter to be sure you will have enough memory available. Use `p20` and `p28` queues as they have 120 GB of RAM memory available. Requested memory with `-l` memory parameter is per requested core (in the example above the system will reserve 80 GB of RAM, 2 x 40GB). `bwa-mem2` doesn't use more then one core. To get more memory for indexing do not increase core number but increase memory.

bwa-mem2.sge

```
#!/bin/bash
#$ -N bwa-mem2
#$ -cwd
#$ -pe *mpisingle 16

module load bioinfo/bwa-mem2/2.2.1

bwa-mem2 mem -t $NSLOTS human_g1k_v37.fasta human_g1k_v37.fasta SRR7733443_1.fastq SRR7733443_2.fastq > d3_align.sam
```