

You need:
A fastq file (provided= Rabbit.fastq) + Reference sequence - you can
download it from:

www.ensembl.org

The screenshot shows the Ensembl website's main navigation and search area. At the top is a dark blue header with the Ensembl logo and links for BLAST/BLAT, VEP, Tools, BioMart, Downloads, Help & Docs, and Blog. Below this is a row of tool categories: Tools (with a link to 'All tools'), BioMart (with a description: 'Export custom datasets from Ensembl with this data-mining tool'), BLAST/BLAT (with a description: 'Search our genomes for your DNA or protein sequence'), and Variations (with a description: 'Analyse function or unknown'). The central search bar is titled 'Search' and contains a dropdown menu set to 'All species', a text input field, and a 'Go' button. Below the search bar, example queries are provided: 'e.g. BRCA2 or rat 5:62797383-63627669 or rs699 or coronary heart disease'. On the left side, under 'All genomes', there is a dropdown menu labeled '-- Select a species --' which is circled in red. Below this menu are two links: 'View full list of all Ensembl species' and 'Edit your favourites'. On the right side, under 'Favourite genomes', there are two entries: 'Human' (GRCh38.p12) with a classical bust icon and a link 'Still using GRCh37?', and 'Mouse' (GRCm38.p8) with a mouse icon.

Select rabbit

Genome assembly: OryCun2.0 (GCA_000003625.1)



[More information and statistics](#)










[Download DNA sequence \(FASTA\)](#)



[Display your data in Ensembl](#)

Other assemblies

-  [Oryctolagus_cuniculus.OryCun2.0.dna.chromosome.8.fa.gz](#)
-  [Oryctolagus_cuniculus.OryCun2.0.dna.chromosome.9.fa.gz](#)
-  [Oryctolagus_cuniculus.OryCun2.0.dna.chromosome.MT.fa.gz](#)
-  [Oryctolagus_cuniculus.OryCun2.0.dna.chromosome.X.fa.gz](#)
-  [Oryctolagus_cuniculus.OryCun2.0.dna.nonchromosomal.fa.gz](#)
-  [Oryctolagus_cuniculus.OryCun2.0.dna.toplevel.fa.gz](#)
-  [Oryctolagus_cuniculus.OryCun2.0.dna.rm.chromosome.1.fa.gz](#)

Choose: `Oryctolagus_cuniculus.OryCun2.0.dna.toplevel.fa.gz`

In unix, to decompress: `gunzip`

`Oryctolagus_cuniculus.OryCun2.0.dna.toplevel.fa.gz`

1)Index the reference:

```
bwa index -a bwtsw Reference.fa
```

#It will create several files in you directory with the same name of the Reference

2) align reads (you can choose between different command, we chose mem because it is indicated for NGS)

```
bwa mem Reference.fa Rabbit.fastq > Rabbit.sam
```

#it creates the alignment file (plain text) that you want to have in binary format

3) Use samtools, as input give the sam files, as output obtain the bam

```
samtools view -bS Rabbit.sam > Rabbit.bam
```

sort and index (also the bam file needs to be indexed) – you need to specify the input and the output name of your new sorted output

```
samtools sort Rabbit.bam Raddit_sorted
```

#will create a new file named Raddit_sorted.bam

```
samtools index Rabbit_sorted.bam
```

#will create Rabbit_sorted.bam.bai

4(index the reference file with samtools (needed for IGV)

```
Samtools faidx Reference.fa
```

At the end you have:

Reference.fa Reference.fa.fai Rabbit_sorted.bam Rabbit_sorted.bam.bai

And they are all needed for using IGV

Check the manual of bwa and samtools and explore other commands. Enjoy. 🐰 For any question: