

# Format Converting Sequences

**Task Name:** convert-seq

Converts a sequence from one format to another.

**Parameters:**

*in* — input sequence file. [String, Required]

*out* — name of the output file. [String, Required]

*format* — format of the output file. [String, Optional]

The following values are available:

- fasta
- fastq
- genbank
- gff
- raw

**Example:**

```
ugene convert-seq --in=human_T1.fa --out=human_T1.gbk --format=genbank
```