

# Adding Phred Quality Scores to Sequence

**Task Name:** join-quality

Adds Phred quality scores to a sequence and saves the result to the output FASTQ file.

**Parameters:**

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

*quality* — input Phred quality scores file. [String, Required]

*out* — output FASTQ file. [String, Required]

**Example:**

```
ugene join-quality --in=e_coli.fa --quality=e_coli.qual --out=res.fastq
```