

# Annotating Sequence with UQL Schema

**Task Name:** query

Annotates a sequence in compliance with a UGENE Query Language (UQL) schema. This allows to analyze a sequence using different algorithms at the same time imposing constraints on the positional relationship of the results.

To learn more about the UQL schemas read the [Query Designer Manual](#).

**Parameters:**

*in* — semicolon-separated list of input sequence files. [String, Required]

*out* — output Genbank file with the annotations. [String, Required]

*schema* — UQL schema. [String, Required]

*merge* — if true, merges regions of each result into a single annotation. [Boolean, Optional, Default: false]

*offset* — if *merge* is set to true, specified left and right offsets for merged annotations. [Number, Optional, Default: 0]

**Example:**

```
ugene query --in=input.fa --out=result.gb --schema=RepeatsWithORF.uql
```