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# MASSCHROQ<sub>3</sub> USER MANUAL

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FREE AND OPEN SOURCE PEPTIDE QUANTIFICATION SOFTWARE

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# I *MASSCHROQ<sub>3</sub>*

## 2 *MASSCHROQ* EXPORT TOOL

*MassChroQ3* comes with a CLI tool *masschroq-export* to extract data from the CBOR *MassChroQ3* output file

*masschroq-export* online help

```
$ masschroq-export -h RETURN
```

### 2.1 EXPORT ALIGNMENT DATA TO JSON

*extracting alignment data to JSON file*

```
$ masschroq-export --json alignment_data.json mcq_quantification_results.cbor RETURN
```

### 2.2 GENERATE PDF ALIGNMENT DATA REPORT USING TYPST

You need the JSON alignment data file generated in [SECTION 2.1 “EXPORT ALIGNMENT DATA TO JSON”](#).

Prepare a simple Typst file (text file with .typ extension) called “alignment.typ” with this content:

```
#import "@preview/teotegraph:0.2.0": *  
  
= Display retention time alignment informations  
  
#let mcq3_json = json("alignment_data.json")  
#mcq3-alignment-summary(mcq3_json)
```

And compile this file using :

*Compile alignment typst file*

```
$ typst compile alignment.typ RETURN
```

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# BIBLIOGRAPHY