

Price List for Aptamer and Phage Library Quality Control

| Quality control of starting libraries: | |
|---|-------------------|
| Number of starting libraries | Price per library |
| 1 | 400 € |
| Up to 6 | 300 € |
| Up to 12 | 260 € |

| Description of content: | |
|--|--|
| Check the distribution of nt over all random region positions | Diagrams and tables with exact values: Allow to assess if libraries meet you expectations (actual vs. planned distribution). |
| Count of full length sequences | Histogram and tables: Allow to assess the frequency distribution of full-length sequences in your library. Most frequent sequences including their counts are indicated. Implementation of user defined databases enables the identification of contaminations, tag binders, separation matrix binders, etc. |
| Check the distribution of random sequence lengths | Histogram that visualizes the distribution of random region lengths: Allows to asses if length of your constructs meets your expectations. |
| Check the distribution of motif frequencies | Histograms and tables: Allow to assess the frequency distribution of motifs of defined lengths. Most frequent sequence motifs including counts are indicated. |

Delivery of all types of results (analysis of screening experiments, QC)

You will receive the analysis as files, which are organized by type in a self-explaining folder structure accompanied by a pdf-document, which exemplarily explains different types of result files/graphs.

Furthermore, you will receive the result files together with our **free** COMPAS viewer software (Windows or Linux). The viewer software enables:

- Zooming into histograms and diagrams to display and interpret NGS data at very high resolution (down to a couple of sequences).
- A dynamic and user defined annotation of identified sequences by the implemented fuzzy-search algorithms.
- Selection and collection of interesting data points (sequences) by a simple mouse click for further investigation (probe selection possible in suitable types of result files).

Results are provided additionally in a format that enables convenient further processing:

- For appropriate result types, we provide csv-files to enable a straightforward import into Excel or other spreadsheet software.
- Results containing sequence lists are provided in FASTA format to be compatible with further data processing by third party software.