

#### **FASTERIS SA**

Chemin du Pont-du-Centenaire 109 CH-1228 Plan-les-Ouates

Switzerland

Phone: +41 22 794 22 23 email: compta@fasteris.com Our VAT: CHE-116.347.036 VAT

University of Leipzig
The Interdisciplinary Centre for Bioinformatics
Dr. Cristian A. Velandia-Huerto
Haertelstrasse 16-18
04107 Leipzig
Germany

Plan-les-Ouates, 05.04.2019

# **Quotation 30140**

Contact: Axel Strittmatter / ht\_seq@fasteris.com

Your Purchase Order: Quotation date: 05.04.2019
Project: Customer: 11721

# Science Exchange request: #108960. This quotation is for small RNA library preparation and sequencing.

Customer will supply to Fasteris 6x total RNA samples derived from *Botryllus schlosseri, Molgula occidentalis* and *Halocynthia roretzi*, all with estimated genome size of less than 800 Mb. Please supply to Fasteris per samples 2-3 µg of total RNA in 10 µl as per the Fasteris specifications.

Fasteris will do 6x illumina TruSeq small RNA library preparation including gel-sizing step on PAGE gel. Standard cutting size is 18-25 nt. Please indicate before the start of project if you prefer another cutting size.

Sequencing of 6x libraries on 1x shared lane run (ECO lane) with 1x50 bp single reads and aiming for 100 mio reads data output.

Delivery of FASTQ data sorted according to indexing.

TAT: For shared lane runs, the FASTQ data from the sequencing run will be ready for download with 4-6 weeks time after successful pass of entry QC for all samples and depending on other customer libraries to share the run. Accordingly, the service time may be extended to max 5-8 weeks.

Service offer is tax-free according to Switzerland export rules. "Einfuhrumsatzsteuer" may be applicable according to German tax rules.

Item	Designation	Unit	Quantity	Unit Price % Disc.	Total
ILE-30	Illumina Sequencing - Library preparation - Standard Protocol small RNA illumina for 1-8 Rx	lib	6	318.18	1'909.08

Transfer to page 2 EUR 1'909.08

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Item Designation Unit Quantity Unit Price % Disc. Total

Transfer from page 1 1'909.08

### This item is linked to the document SP-RNA-Small-201610.pdf Sample requirements:

- Purified total RNA at the following concentration: 3 ug, in a total volume of 10 uL.
- Suspension buffer: Tris or water
- NB! DNase treatment must be done in your lab
- If sample number exceeds 8, samples must be plated by column in 96 well plates
- ADDITIONAL FEES WILL APPLY IF SAMPLES ARE NOT AT THE CONCENTRATION AND VOLUME SPECIFIED ABOVE

## **Shipping conditions:**

- The copy of the quote and completed order form **MUST BE ENCLOSED** to the parcel
- Electronic version of the completed order form must be sent also by e-mail
- Samples must be sent on dry ice
- Bioanalyser of equivalent profiles of the samples should be provided

## Library preparation procedure:

- Initial Quality Control: Checking the concentration and quality of the samples
- Polyacrylamide gel size selection of 18-30 nucleotides
- Library preparation using illumina TruSeq small RNA kit
- Library Quality Control:
  - 1. Library dilution at 10nM

If customer-supplied samples or libraries are not within the Fasteris specifications, we cannot foresee or guarantee the analysis results. In case of failure, all experimental work, all so far library preparation steps and/or all sequencing performed accordingly will be charged.

Lane

IRN-02 Illumina Sequencing - Run - NextSeq

Single-reads, 1x 50 bp 100 M ECO lane

About 100 million reads or 5 Gb Expected Q30 min 85%\*

Fasteris bank address:SubtotalEUR2'727.26Banque Raiffeisen du SalèveVAT0.0 %2'727.260.00

1255 Veyrier Switzerland

Account owner: FASTERIS SA

SWIFT: RAIFCH22

IBAN: CH12 8018 7000 0222 8118 6 Total EUR 2'727.26

Payment: 30 DAYS NET

Please contact us if you wish to pay with credit cards.

Thank you for your order

VISA 

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818.18

By sending samples to Fasteris, you agree with our Terms and Conditions and you are placing an order.

A Purchase Order (PO), including PO number and billing address, has to be provided with the order form by email and also paper copy in the parcel. Please carefully follow the instruction on the order form (for sample registration).

Please note that any later change of order confirmation details, including billing address changes, may cause additional administration fees.

This quote is valid 2 months.

<sup>\*</sup>Specified values are obtained with genomic libraries with balanced sequence diversity. These values do not apply for ready-to-run or low sequence diversity libraries.