

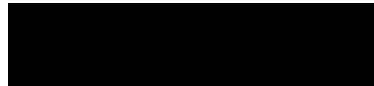
**Next-generation sekvenování****Odběratel:**

Univerzita Palackého v Olomouci
Křížkovského 511/8
77900 Olomouc
Česká republika

Reg. No.: 61989592
DIČ: CZ61989592
E-mail: [redacted]

Příjemce:

Katedra buněčné biologie a genetiky,
PřF

**Dodavatel:**

SEQme s.r.o.
Dlouhá 176
263 01 Dobříš
Reg. No.: 24312819
DIČ: CZ24312819
E-mail: [redacted]

Datum vystavení: 10.04.2024

Vaše číslo objednávky: -

Protokol: NGS - Illumina - Sekvenování na
zakázku

Doručení: **Kurýrní služba**

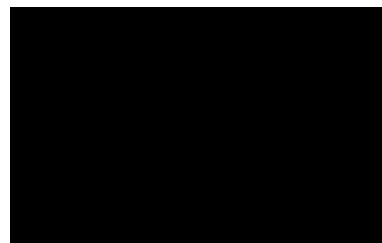
Datum vyzvednutí vzorků: **12.4.2024**

Popis

mRNA knihovna (LP-060)
ShareSeq Data Package, PE150, 100 million reads / 15 Gb (DP100-PE150)
Bioinformatické služby, paušál na zakázku (BS-SB)
Doručení - Kurýrní služba
Bioinformatic/Laboratory services, daily rate (BS-DR)

Množství

6 x
2 x
1 x
1 x
1 x

Celkem k úhradě včetně DPH:**98 300,40 CZK****Na analýzu zasílám:**

- 6 zkumavek

Doporučujeme používat 8-zkumavkové stripy s individuálními víčky (např. Eppendorf 0030124359) nebo 96-jamkové destičky uzavřené víčky. Nepoužívejte parafilm. Prosíme o jednoduché značení zkumavek nejlépe číslem označujícím pořadí vzorku v objednávce.

Prosíme o uvádění našeho čísla zakázky při veškeré korespondenci s námi.

Firma je zapsaná v Obchodním rejstříku, vedeném Krajským obchodním soudem v Praze, oddíl C, vložka 195507
Objednáním našich služeb nebo zboží souhlasíte s našimi Všeobecnými obchodními podmínkami, které jsou v platném znění k dispozici na adrese www.seqme.eu.

Na analýzu zasílám:

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#	Název vzorku	Koncentrace	Objem
1	UT_1	67 ng / μ l	20 μ l
2	UT_2	70 ng / μ l	20 μ l
3	UT_3	85 ng / μ l	20 μ l
4	FKK6_1	100 ng / μ l	20 μ l
5	FKK6_2	70 ng / μ l	20 μ l
6	FKK6_3	70 ng / μ l	20 μ l

Addendum to Order Confirmation - Please read this document carefully!

YOUR CONSENT

- By **submitting samples for analyses** you agree to all terms and conditions listed including also our General Terms and Conditions.
- If you do not wish to process your samples according to rules specified in this whole document, please do not submit them for analyses and contact us in order to cancel your order.

SAMPLE REQUIREMENTS

- When sending samples for Next-Generation sequencing service, you must follow our Sample Submission Guidelines (SSG). If the conditions set there are not met your samples may not pass our quality control (QC), their sequencing analysis will not be feasible and/or will be delayed until new samples are provided or until we receive your consent to proceed with the existing material.
- Please kindly notice that if your samples do not pass our QC, additional costs for steps taken may be charged. For libraries prepared using samples which have not passed our QC or if customer-prepared libraries are supplied, the technical specifications quoted are considered invalid and the service will be provided at your own risk and invoiced as quoted.
- The sequencing service is carried out under S1 biosafety conditions. Samples submitted must comply with biosafety S1 classification.

SAMPLE SHIPMENT

- If you select sending samples by the courier service, please be aware that samples are transported by external courier services. We are not responsible for any loss of the shipment during transport, delay in its delivery or damage to the shipment before the shipment is properly delivered! The shipment is not insured.
- Depending on where you ship samples from, you may receive additional instructions!

TECHNICAL LIMITATIONS

- Please be aware that due to certain technical limitations, there is always a risk that even when your samples pass our QC the technical specifications quoted (namely read length and count/quality of reads) may not be achieved. This is because the QC test only assesses nucleic acid quantity, integrity and purity (to a certain degree) but does not assess other unrevealable factors e.g. base composition that might negatively affect the outcome of analyses.
- Similarly, library pooling is always performed with due care in order to achieve uniform read distribution but still the count of reads obtained per every pooled library may vary significantly.
- Our sequencing specifications for Illumina sequencers are set using a balanced genomic DNA library since Illumina algorithms are optimized around a balanced representation of ACGT nucleotides. Any divergence from equal base distribution will have a negative impact on the amount and quality of data. Therefore, for samples with low diversity or unbalanced base composition (e.g. amplicons or bisulfite converted samples) a PhiX spike-in will be added to increase the diversity and improve the sequence quality. The exact quantity of a PhiX spike-in used and consequently % of reads that will be represented by the PhiX control library depend on individual sample and sequence characteristics. Please see the Illumina website for details.

STORING OF SAMPLES AND RESULTS

We store samples, sequencing products and results and other data at least for the period specified in the table below:

Samples	At least 3 months starting from the date when we send you a final email confirmation about finishing processing of your order.
Intermediate products of sample processing	Discarded immediately.
Sequencing libraries and library pools	At least 3 months starting from the date when we send you a final email confirmation about finishing processing of your order.
Results and other data	At least 4 weeks starting from the date when we send you a final email confirmation about finishing processing of your order.

It is strongly recommended that immediately after you download results of analyses (or receive them on a USB flash drive), you create a backup copy of it which you will not manipulate with.

BIOINFORMATIC SERVICES

- Total processing time of a particular bioinformatic procedure depends heavily on amount and nature of analyzed data and analysis pipeline used and can only be estimated.

- Data processing is performed with carefully chosen parameters and using the best suitable software. We encourage you to contact us for details in case of need.
- Any special request for using a particular software, setting specific parameters or deviation in analytic pipeline must be discussed and considered beforehand.

IMPORTANT LINKS:

- Sample Submission Guidelines: <https://www.seqme.eu/documents/ngs-ssg-en.pdf>
- General Terms and Conditions: <https://www.seqme.eu/documents/gtc-en.pdf>
- Sample Submission Sheet: <https://www.seqme.eu/documents/sample-submission-sheet-en.xls>
- FAQs: <https://www.seqme.eu/next-gen-sequencing/instructions>

DELIVERY OF RESULTS

- Delivery time of raw data is approx. 6 weeks from the day the samples pass our QC check.
- Data are delivered online via a secure access account unless a USB flash drive (non-returnable) for data delivery is ordered.

DISCLAIMER

- Prices in this order confirmation are valid only if all samples are provided in sufficient quality and quantity within 1 month starting from the date of its issue. If total number of samples is not delivered within that timeframe we reserve the right to withdraw from the contract.
- We reserve the right to invoice steps taken for individual sample processing and/or partial data delivery.
- Please notice that due to the fast technical development it might be possible that between the date of issue of this order confirmation and project start (delivery of samples) technical specifications stated in this document may change. We reserve the right to perform sample analysis by means of employing similar services with comparable outcomes.