

CENOVÁ NABÍDKA

Odběratel: Biofyzikální ústav AV ČR, v. v. i. Královopolská 135 612 65 Brno DIČ: CZ68081707 IČ: 68081707	Příjemce: Biofyzikální ústav AV ČR, v. v. i. ████████████████████ Kralovopolská 135 612 65 Telefon: 541517230 E-mail: ██████████	Dodavatel: SEQme s.r.o. Dlouhá 176 263 01 Dobříš Česká republika IČ: 24312819 DIČ: CZ24312819 E-mail: info@seqme.eu
Nabídka č.: 19NA225 Datum zápisu: 11.07.2019 Platno do: 11.08.2019		

Vážený pane ██████████,
na základě Vaší poptávky Vám tímto nabízíme následující sekvenační služby:

Kód	Popis	Množství	J.cena	Kč Cena
LP-110	gDNA library (size selection included) - PacBio	3 x	21 100	63 300,00
DS-200	PacBio, Sequel SMRT Cell 1M v3 LR (20 hrs movie), 500-600 thousand reads	1 x	72 100	72 100,00
Součet položek				135 400,00
NABÍDKOVÁ CENA CELKEM BEZ DPH			Kč	135 400,00

Nabídka zahrnuje: Výše definované sekvenační služby a dodání hrubých dat ve formátu PacBio, ROI ve FASTQ a CCS ve FASTQ.
Nabídka nezahrnuje: Náklady na doručení vzorků, analýzu dat.

Termín provedení/dodání: Dohodou

Vystavil: ██████████

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

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

Quote Addendum - Please read this document carefully

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 if approved by you 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.

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 number 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 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 number 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.

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. Any special request for using a particular software, setting specific parameters or deviation in analytic pipeline must be discussed and considered beforehand.
- Data are delivered online via a secure access account unless a USB flash drive (non-returnable) for data delivery is included.

DELIVERY TIME

- Delivery time is typically three to six weeks from the day the samples pass our QC check.
- The delivery time is only approximate unless agreed otherwise.

STORING OF SAMPLES AND RESULTS

We store samples, sequencing products and results and other data at least for the period specified 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 30 days 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.

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 issue of this order confirmation.
- 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.

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.

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>
- FAQs: <https://www.seqme.eu/next-gen-sequencing/instructions>
- Glossary of Next-Generation sequencing terms: <https://www.seqme.eu/magazine/glossary>