

CENOVÁ NABÍDKA

Odběratel: Biologické centrum AV ČR, v. v. i. Branišovská 1160/31 370 05 České Budějovice DIČ: CZ60077344 IČ: 60077344	Příjemce: Entomologický ústav [redacted] E-mail: [redacted]	Dodavatel: SEQme s.r.o. Dlouhá 176 263 01 Dobříš Česká republika IČ: 24312819 DIČ: CZ24312819 E-mail: info@seqme.eu
Nabídka č.: 23NA237 Datum zápisu: 29.06.2023 Platno do: 29.07.2023		

Specifikace:

Příprava knihoven a sekvenace houbového ITS (internal transcribed spacer) regionu.

Součástí služby je vyzvednutí vzorků na adrese zadavatele, příprava knihoven včetně kontroly kvality vzorků a připravených knihoven, sekvenace v módu alespoň 2x250 bp, výstup na vzorek alespoň 60k read pairs/sample, bioinformatická analýza včetně taxonomického zařazení detekovaných OTUs, a výsledky sdílené na cloudovém úložišti.

Kód	Popis	Množství	J.cena	Sleva	Kč Cena
SO-048D	Metagenome profiling, up to 48 samples, >120K reads/sample	1 x	[redacted]	[redacted]	[redacted]
SO-192B	Metagenome data analysis, up to 190 samples	1 x	[redacted]	[redacted]	[redacted]
Součet položek					63 720,00
NABÍDKOVÁ CENA CELKEM BEZ DPH					Kč 63 720,00

Nabídka zahrnuje: Výše definované sekvenační služby a dodání hrubých dat. Detailní specifikaci sekvenačních služeb naleznete rovněž na našich webových stránkách.

Nabídka nezahrnuje: Náklady na doručení vzorků a analýzu dat pokud nejsou výslovně zmíněny výše.

Termín dodání výsledků: Dohodou

Vystavil:

Email: [redacted]

Phone: [redacted]

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

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 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 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

- All orders of laboratory and bioinformatic services must be submitted on line using our website www.seqme.eu unless agreed otherwise.
- 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 quote 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.