

Offerta	QUO-20240331	14/06/2024
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DESTINAZIONE	DESTINATARIO
	110301/1885 Università degli Studi di RomaLa Sapienza Dipartimento di Psicologia Via dei Marsi,78 ROMA RM ITALIA

PAGAMENTO	CIG/CUP	PARTITA IVA/CODICE FISCALE	RIFERIMENTO PROGETTO:
B.B. 30 GG. D.F.		PARTITA IVA IT02118311006 CODICE FISCALE 80054330586	prof.ssa Tiziana Pascucci

Codice	Descrizione	U.M.	Quantità	Listino	Sconto	Prezzo	Importo	Aliq.IVA
TSS.RNA.XM.PE150	mRNA-seq, 30M di sequenze accoppiate da 150bp	NR	32	145,00		145,00	4.640,00	22
BIO.DE.STD.024	Produzione tabelle FPKM e analisi di espressione differenziale	NR	32	34,00		34,00	1.088,00	22
DATA.TIER2	Stoccaggio, backup e consegna dati per 500M-4000M reads	NR	1	150,00		150,00	150,00	22

Tutti i prezzi si intendono al netto dell'I.V.A.	TOTALE IVA ESCLUSA
	EUR 5.878,00
Scadenza preventivo: 13/08/2024	TOTALE IVA INCLUSA
	EUR 7.171,16

General Terms and Conditions

Version: Rev04 (valid from October 13th, 2022)



Purchase order

The Customer must send the purchase order to orders@igatechnology.com before samples are shipped.

Samples

Samples should be shipped along with a hard copy of the compiled Samples Spreadsheet (available on www.igatechnology.com), providing the quote reference, contact person, and mandatory information of samples. The samples must meet the quality and quantity criteria, and the shipping conditions, as indicated inside each application-specific "Sample Requirements" document on our website. In case such specifications are not available the Customer shall enquire before sending any material. If storing or shipping conditions or sample specifications do not meet the required standards, IGA Technology Services may ask for an additional processing fee and the standard turnaround time will be delayed. The Customer will be alerted in case of any non-compliance during the sample QC and will have to decide whether to carry out the service anyway or to replace non-compliant samples/libraries. Additional fees may be applied for extra sample manipulation, QC, or library preparation. In case the Customer decides to proceed with the processing of non-compliant samples, IGA Technology Services will not be responsible for any partial or total failure of the experiment. In case the Customer decides not to proceed, only the sustained handling costs will be charged. If the sequencing of non-compliant samples results in insufficient data quality/quantity, IGA Technology Services will not take responsibility to provide extra services and the full price will be invoiced. Processed biological samples and any unused sample (back-up, QC failed one, etc.) will be kept for 3 months following the data delivery and then discarded. Sample restitution can be requested by and no later than 3 months from the delivery results. Shipment should be arranged and purchased independently by the Customer in agreement to IGA Technology Services ensuring that appropriate packaging and refrigeration are considered. Courier's box arrival and pickup scheduling should be agreed upon with IGA Technology Services' staff with a minimum of 5 working days in advance. For optional long-term sample storage please contact IGATech for pricing and availability.

Sequencing yields

The standard quality policy is set to a minimum of 95% of target sequencing output (expressed in millions of reads or Gbps). Samples satisfying this threshold will be considered as completed unless agreed differently before the order is placed. This threshold applies to sample-by-sample experiments (i.e., where each sample is barcoded separately and manipulated independently), it does not apply to pooled-samples experiments; this may include, but not limited to, ddRAD genotyping, Allegro genotyping, custom target enrichment, where a minimum 85% yield threshold is considered on the aggregated value of each pool depending on the strategy adopted. Sample-to-sample sequencing yield variability can be expected in pooled approaches, and this can be caused by DNA quantity and uniformity, presence of inhibitors, DNA degradation. IGA Technology Services is not responsible for those factors. A normalization service may be provided to compensate variability in the quantity of DNA; this however will not guarantee a perfect uniformity. For 16S, 18S, ITS, or other amplicon-based metagenomics/metabarcoding/genotyping applications, samples are directly processed through PCR amplification and library preparation. Successful library amplification will be used as only a QC checkpoint. If some samples within a batch fail the amplification, while others succeed, the failure is deemed to be caused by a lack of template DNA or PCR inhibitors, and IGA Technology Services is not obliged to repeat the experiment. Concentration values provided by the customer will be utilized for PCR set-up; if the customers declared values that are out of specifications or significantly different from what was declared, IGA Technology Services will be not responsible for any lack of results or adequate quality and quantity of sequencing data. Only successful libraries will be sequenced, regardless of the outcome of other libraries in the batch and the whole work order will be charged in full. IGA Technology Service may credit to the customer unused sequencing value to further experiments.

Customer-provided libraries

Customers submitting libraries ready to be sequenced (i.e., already containing the due multiplexing indexes) must provide complete and correct information on index sequences used, as well as kit references (or adapter sequences along with custom protocol). All data must be reported in the "Library" sheet of the "Sample Spreadsheet" form. Note that erroneous information may lead to barcode collision or may hamper the successful sequencing due to sample misassignment, thus IGA Technology Services will be not responsible for any data loss, and the experiment will be fully charged regardless of its outcome. If any inconsistency in the information is found or the standard library QC/quantification fails, IGA Technology Services has the discretion to refuse to continue with the experiment, and only QC fees will be applied. IGA Technology Services is not responsible for sequencing failures due to library preparation, oligo/adaptor, or indexing that are not compatible with the chosen sequencing platform.

Sequencing optimization

Should the service require only the partial use of a sequencing flow-cell, the samples will be processed when the remaining capacity of the flow-cell is fill up by the samples of other Customers. To ensure higher quality service to its customers, IGA Technology Services may load a test pool on a flow cell and evaluate the results before sequencing the whole amount requested in the project. In any case, IGA Technology Services will not be responsible for delayed deliveries or services canceled due to force majeure or, in any event, factors beyond its control, such as technical problems with the instrumentation or delays in the delivery of the reagents by the suppliers.

Pseudonymization

Any sample of human origin, including but not is limited to DNA, RNA, blood, tissue, saliva, stool, must be provided in pseudonym form. This means that all personally identifiable information must be REMOVED and not available to IGA Technology Services (this may include, but is not limited to, name, surname, date of birth, fiscal code, etc.). Means of transmission include, but are not limited to mail, Sample Spreadsheet, shipped envelopes, or direct labeling of tubes. Reception of samples along with any sensitive data will hamper the ability to sequence them. The client will be requested to provide new sample identification in a pseudonymized form. IGA Technology Services will be responsible to destroy any personal information related to the samples. If pseudonymization (or destruction of information) is not possible due to direct labeling of sample containers with personal data, these will be shipped back to the sender. Non-personal data which might be used for the only scope of the analysis (e.g., age, weight, prognosis, sex, drug treatment, etc.) can be submitted through the Sample Spreadsheet without limitations.

Communications

All requests for information about the service must only be sent via email (orders@igatechnology.com) and will be dealt within 2 working days from receipt. In the event problems arise during the processing, the Customer will be contacted directly to agree on possible solutions. Otherwise, the Customer will only be contacted at the end of the service. Notifications will be sent to the contact person indicated in the Sample Spreadsheet form at sample reception, QC results, and delivery.

Delivery times

Our standard data delivery time is between 6 and 10 working weeks, depending on the type of service required, the need for specific data analysis, and the optimization of the use of the Illumina platform, as described below. The time will be counted from the sample QC date until data is delivered. In case some samples fail the incoming QC, and a replacement is requested, time will be counted once the new samples pass the incoming QC. Alternatively, the customer must send a written (e-mail) communication with acceptance to proceed with sample analyses despite the quality requirements that are not met. Samples requiring nucleic acids extraction may require additional time for processing depending on the complexity/difficulty/scarcity of the incoming samples. Any delay caused by these factors is not the responsibility of IGA Technology Services. For projects involving protocol customization, custom reagents orders, or the development of dedicated protocols, the time for data delivery will be agreed upon with the client on a project basis. Shorter turnaround times are available on request, and they must be agreed in advance and specified within the quotation.

Data storage and delivery

At the end of the service, the data will be made available to the Customer on a SFTP/web server of IGA Technology Services for the minimum period of two weeks after the receipt of the delivery notification. The Customer will receive a username and personal password to access the data. The Customer may request the delivery of the data via a hard drive, sustaining the associated additional costs. The raw and processed data will be retained on IGA Technology Services' servers for 3 months, starting from the date of delivery. After this period, data will be deleted without notification. If extended persistence is required, it must be notified beforehand (within 2 months from data delivery). Extra charges will be applied for extended storage. After download, the customer is responsible for checking data integrity by the provided MD5 files. IGA Technology Services will not consider any claim on data integrity or availability after 3 months from the delivery date.

Confidentiality and Privacy Policy

All customer information is held with strict confidence. All materials and information sent to, and the data produced by IGA Technology Services for a given order are the exclusive property of the customer and will be returned to the customer or discarded confidentially. Unless agreed in a different contract, the Customer assigns and agrees to assign to IGA Technology Services all rights in Italy and throughout the world to inventions, discoveries, improvements, ideas, designs, processes, techniques, strategies, products, substances, computer programs, databases, trade secrets, know-how, information, data, documentation, reports, research and other creations arising or derived from or made in the performance of the service. Customer data may be used for marketing activities only when agreed with the customer. For the customer's privacy policy, please retrieve the latest document available at the following link: <http://www.igatechnology.com/igatech/documents>.

Bioinformatics Services and Outputs

All the standard analyses and sequencing delivery include either raw data or adapter-masked data. Standard applications which are executed with regular adapter included via ligation and not carrying specific features are by default provided with masking of any adapter read-through (masked by Ns). Libraries such as those providing UMIs, linked-reads barcodes, deduplication, or any other sequences generated by specific primer-extension may be delivered as pure raw data since any masking or trimming may impact the performance of downstream analyses that we are not controlling. Please consult the application-specific "Data Delivery Specification" on our website (or inquire if not present) to learn about each application delivery format. Quality control reports will be provided for any read set (excluding sequencing indexes). Data will be always provided as base-called and demultiplexed. Raw signals will be not provided unless previously agreed. Samples that are sequenced on multiple lanes/runs may be provided as separated files. Data integration may request an extra service fee.

Billing

For EU and UK customers, orders of net amounts less than 10,000 EUR, invoicing will take place at the end of the service. For orders of net amounts equal to or greater than 10,000 EUR, invoicing will take place in two stages: 50% on receipt of the samples and 50% at the end of the service. For all other countries, orders of net amounts less than 5,000 EUR, invoicing will take place on receipt of the samples, while orders of net amounts equal or greater than 5,000 EUR, invoicing will take place in two stages: 50% on receipt of the samples and 50% at the end of the service. For delayed due payments IGA Technology Services may ask extra fee within the limit of 5% of invoice value per month of delay. Should the service not be successful due to internal technical problems, it will be repeated without any additional charges to the Customer. Should the service not be successful on two rounds of preparation or sequencing, 50% of the amount of the order will be invoiced in any case to partially cover the costs sustained.