

Purchase order. Before samples are shipped a purchase order must be sent to orders@igatechnology.com or loaded in the assigned project area accessible at customer-portal.igatechnology.com.

Samples

Submission Requirements. All samples must be accompanied by the Samples Spreadsheet, available in the GUIDELINES section at igatechnology.com. This spreadsheet should include the quote reference, client contact information, and detailed sample descriptions. Samples must adhere to the quality, quantity, and shipping conditions outlined in our "Sample Requirements" documents. If there is any uncertainty, please seek clarification before sending your samples.

It is crucial to understand that the guidelines and thresholds detailed in the application-specific "Sample Requirements" documents, available in the GUIDELINES section or through the CUSTOMER-PORTAL, are a fundamental part of our Terms and Conditions (including Shipping Conditions). These guidelines may supersede the stipulations mentioned herein. Clients must read the Sample Requirements, which are accessible on igatechnology.com, or request a copy. Adhering to these requirements is essential to ensure the quality and success of your sequencing projects.

Non-Compliant Samples. IGA Technology Services reserves the right to impose additional charges and extend processing times for samples that do not meet the specified standards or arrive in inadequate shipping conditions. Clients will be notified upon sample arrival and after quality control (QC) if their samples are deemed non-compliant. At this point, clients must decide whether to proceed with the non-compliant samples—understanding that this releases IGA Technology Services from any liability for experimental failures, such as unsuccessful library preparation or low sequencing output due to poor sample quality—or submit replacement samples, which may result in additional fees and/or an extended Turn-Around Time (TAT). Clients who choose not to proceed with the non-compliant samples will be billed only for handling costs. If sequencing is performed on non-compliant samples and results in poor data quality or quantity, the full service fee will still be charged.

Sample Storage and Return. Processed and unused samples are stored for three months after delivery. After this period, samples will be discarded. Clients must request the return of samples within this timeframe. Clients are responsible for all shipping costs and arrangements, including ensuring proper packaging and refrigeration. Courier scheduling must be arranged at least five working days in advance with IGA Technology Services. For long-term storage options and pricing, please contact IGATech.

Sequencing yields. Our standard quality policy mandates a minimum of 95% of the targeted sequencing output, measured in millions of reads or Gbps. Samples that meet or exceed this benchmark will be considered successfully completed, unless a different standard is agreed upon prior to placing the order. This policy applies specifically to experiments conducted on a sample-by-sample basis, where each sample is individually barcoded and processed. However, it's important to note that this output guarantee does not extend to long-read sequencing technologies, such as Oxford Nanopore or Pacific Biosciences, due to the inherent variability in sample quality these methods may encounter. For custom pooled-sample experiments, which might include, but are not limited to, genotyping-by-sequencing and custom target enrichment techniques, a minimum yield threshold of 85% is established based on the aggregated value of the final enriched pool expected yield. Variability in sequencing yield from one sample to another is expected in pooled sample approaches, influenced by factors such as DNA amount and uniformity, the presence of inhibitors, and DNA degradation. IGA Technology Services assumes no responsibility for variability caused by these factors. While we offer a DNA quantity normalization service to help mitigate variability, we cannot guarantee absolute uniformity in the sequencing results.

Customer-provided libraries. Customers submitting libraries ready for sequencing, complete with necessary multiplexing indexes, must provide accurate and comprehensive details regarding the index sequences utilized. This includes references for the kits or adapter sequences and any custom protocols employed. All this information must be meticulously recorded in the "Libraries-Spreadsheet" form. Incorrect information can lead to barcode clashes or misassignment of samples, impairing successful sequencing. Consequently, IGA Technology Services will not be held accountable for any data loss, and the full cost of the experiment will be invoiced, regardless of the outcome. If discrepancies in the provided information are identified, or if the standard library QC or quantification procedures fail, IGA Technology Services reserves the right to hold the experiment, applying only the QC charges. Furthermore, IGA Technology Services disclaims any responsibility for sequencing failures arising from issues related to library preparation, oligos/adapters, or indexing that are incompatible with the selected sequencing platform.

Pseudonymization. Any sample of human origin, including but not limited to DNA, RNA, blood, tissue, saliva, stool, must be provided in pseudonym form. This means all personally identifiable information must be REMOVED and not available to IGA Technology Services. This includes, 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. Receiving samples with any sensitive data will hinder our ability to sequence them. The client will be requested to provide a new sample identification in a pseudonymized form. IGA Technology Services will be responsible for destroying 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 that might be used solely for the purpose of the analysis (e.g., age, weight, prognosis, sex, drug treatment, etc.) can be submitted through the Sample Spreadsheet without limitations.

Communications. All inquiries regarding the service must be directed via email, either to the assigned specialist or a commercial contact. Specific contact emails are provided in the Sample Requirements documents. If these contacts are not known, please use the default address: orders@igatechnology.com. Should any issue arise during the processing phase, IGA Technology Services will reach out directly to the

customer to discuss and agree upon potential resolutions. Updates, including those related to sample receipt, quality control (QC) outcomes, and final delivery, will be communicated to the contact person designated in the Sample Spreadsheet form.

Delivery times. The time to complete a service varies with the service type, sample volume, and sequencing depth required. Clients desiring specific timelines should mention this during the quote stage. Typically, standard projects involving library preparation, sequencing and bioinformatics service take about 6-8 weeks. Additional time may be required for extraction or large sequencing volumes. If samples fail initial QC, causing a delay until replacement samples pass QC, Clients can authorize proceeding with non-compliant samples via email. Complex nucleic acid extraction may extend processing times, with IGA Technology Services not responsible for such delays. Custom projects, including those requiring specific protocols or reagents, will have timelines agreed upon with the Client. Requests for faster processing should be discussed and included in the quote.

Data storage and delivery. Upon completion of the service, IGA Technology Services will host the data on a SFTP/web server, making it accessible to the customer for four weeks following the delivery notification. Customers will be granted a unique username and password to retrieve their data. If preferred, customers can opt to receive data via a hard drive, covering any related additional costs. Both raw and processed data are preserved on the servers of IGA Technology Services for three months from the delivery date, after which they are permanently deleted without further notice. Requests for data retention beyond this period must be communicated in advance, specifically within two months from the date of data delivery and will incur additional charges for the extended storage service. It is the customer's responsibility to verify the integrity of the downloaded data using the provided MD5 files. Any concerns regarding the integrity or availability of the data raised more than three months after delivery will not be entertained by IGA Technology Services.

Confidentiality and Privacy Policy. IGA Technology Services holds all customer information in the highest confidence. Every piece of material, information sent, and data produced for a given order remains the exclusive property of the customer. Such items will either be returned to the customer or disposed of in a confidential manner. Unless stipulated by an alternative agreement, the customer conveys and concurs to transfer to IGA Technology Services all rights, applicable in Italy and globally, to any inventions, enhancements, concepts, designs, methods, techniques, strategies, software, databases, expertise, and other innovations developed during the service execution. The use of customer data for marketing purposes is contingent upon explicit consent from the customer, which can be revoked at any time, barring instances where a distinct contract dictates otherwise. To review the most current version of our customer privacy policy, please visit <http://www.igatechnology.com/documents>.

Bioinformatics Services and Outputs. All the standard analyses and sequencing delivery include either raw data or adapter-masked data. Libraries that provide UMIs, linked-reads barcodes, deduplication, or any other sequences generated by specific primer-extension may be delivered as pure raw data, as masking or trimming could impact the performance of downstream analyses conducted by third-party software. Data will always be provided as base-called and demultiplexed. Raw signals will not be provided unless previously agreed upon. Samples sequenced on multiple lanes/runs may be provided as separated files and data integration may require an extra service fee.

Billing. Billing practices for IGA Technology Services vary based on the customer's location and the net order amount. For EU and UK customers, invoices for orders of less than 10,000 EUR are issued upon service completion. For orders of 10,000 EUR or more, billing is divided into two parts: 50% upon receipt of the samples and the remaining 50% upon service completion. Customers from other countries will be invoiced upon sample receipt for orders less than 5,000 EUR. For orders of 5,000 EUR or more, the invoicing process mirrors that of the EU and UK, with 50% due at sample receipt and the remainder at the end of the service. Should there be any delays in payment, IGA Technology Services reserves the right to impose an additional charge, up to a limit defined by the EU Directive 2000/35/EC and implemented in the Italian Legislative Decree No. 231 of 9 October 2002. Prices quoted are based on the volume of samples submitted and the associated economies of scale. If the customer submits a significantly lower number of samples than initially agreed upon, the unit price will be adjusted based on standard list price or the order will be due in full. Similarly, if the agreed quantity of samples is delivered in multiple batches not initially planned for, these will incur a different rate compared to a single-batch submission estimated in the quotation, unless a multi-batch processing agreement was previously established.