



Sample submission guidelines

Get your samples ready for success.

Quality nucleic acid input is what makes quality data output possible. These guidelines cover packaging, labeling, shipping and the minimum sample requirements for every service, so your project starts on the right foot.

Measure by fluorometry

All quantities assume Qubit, Picogreen or RiboGreen. If you measured on a spectrophotometer such as a Nanodrop, increase concentrations by roughly 2x.

Match the form to the tubes

Sample names and quantities on the Sample Submission Form must match the tube labels exactly. Email the form and any QC data ahead of arrival.

Tell us before you ship

Send the form and the tracking number by email. We cannot receive packages at weekends, so time the shipment to arrive on a weekday.

Quotes and ordering

sales@omics4.com
+33 7 69 44 16 18

Samples, protocols, QC

lab@omics4.com
+33 4 13 73 24 81

Laboratory

Méditerranée Infection building
13005 Marseille, France

Full guidelines

[omics4.com/
sample-submission-guidelines](https://omics4.com/sample-submission-guidelines)

DNA sequencing service sample requirements

DNA can be submitted in DNase-free water, elution buffer, or 10 mM Tris pH 8.0. Samples should be RNase-treated, show no degradation or contamination, and have an OD260/280 as close to 1.8 to 2.0 as possible. Ship with ice packs.

Concentration note. Values below assume fluorometry (Picogreen, Qubit, RiboGreen). If you are relying on spectrophotometry such as a Nanodrop, increase concentrations by roughly 2x.

Illumina services: DNA

Service	Sample type	Recommended	Minimum	Min. concentration
Whole Genome Sequencing	Genomic DNA	≥ 500 ng	200 ng	10 ng/μL
Whole Genome Sequencing (PCR-free)	Genomic DNA	≥ 1 μg	500 ng	20 ng/μL
Whole Exome Sequencing	Genomic DNA	≥ 500 ng	100 ng	10 ng/μL
Complete Plasmid DNA Sequencing	Plasmid DNA	≥ 1 μg	500 ng	20 ng/μL
Viral Genome Sequencing	Genomic DNA	≥ 1 μg	500 ng	20 ng/μL
Amplicon Sequencing	Purified amplicon	≥ 1 μg	500 ng	20 ng/μL
GBS / ddRAD	Genomic DNA	≥ 300 ng	100 ng	10 ng/μL
Metagenome Sequencing	Metagenome DNA	≥ 500 ng	20 ng	5 ng/μL
16S / 18S / ITS Sequencing	Genomic DNA	≥ 100 ng	10 ng	1 ng/μL
SSR Genotyping	Genomic DNA	≥ 500 ng	200 ng	10 ng/μL
HLA Typing	Genomic DNA · cells/PBMC · blood · buccal swab · DBS	≥ 200 ng · ≥ 1×10 ⁶ · ≥ 1 mL · 2 swabs · 2 spots	—	—
TCR-Seq	Genomic DNA · PBMC · animal tissue · blood	≥ 2 μg · ≥ 2×10 ⁵ · ≥ 500 mg · ≥ 0.5 mL	—	20 ng/μL

Long-read platforms: PacBio and Nanopore

Higher input requirements than short-read Illumina services. Plan for a larger extraction volume if this is your target platform.

Service	Sample type	Recommended	Minimum	Min. concentration
Whole Genome Sequencing (PacBio)	Genomic DNA	≥ 3 μg	—	80 ng/μL

Service	Sample type	Recommended	Minimum	Min. concentration
Whole Genome Sequencing (Nanopore)	Genomic DNA	$\geq 5 \mu\text{g}$	—	20 ng/ μL
Plasmid Sequencing (Nanopore)	Genomic DNA	$\geq 1 \mu\text{g}$	500 ng	10 ng/ μL
Full-Length 16S / 18S / ITS Amplicon	Genomic DNA · tissue · thallus · interstitial fluid · environmental	$\geq 500 \text{ ng} \cdot 1\text{--}3 \text{ g} \cdot 5 \text{ g} \cdot 3\text{--}5 \text{ mL} \cdot 3\text{--}5 \text{ g}$	1 g · 3 g · 1 mL · 1 g	10 ng/ μL
Long-Read Metagenomic Sequencing	Genomic DNA · tissue · fluid/ sediment · environmental	$\geq 2 \mu\text{g} \cdot 2 \text{ g} \cdot 6\text{--}10 \text{ mL} \cdot 6 \text{ g}$	1 g · 2 mL · 2 g	30 ng/ μL

Epigenomics

Service	Sample type	Recommended	Minimum	Min. concentration
ATAC-seq	Cells · tissue	$\geq 1 \times 10^6 \cdot \geq 500 \text{ mg}$	$5 \times 10^4 \cdot 200 \text{ mg}$	—
MeDIP-seq / hMeDIP-seq	Genomic DNA	$\geq 2 \mu\text{g}$	1 μg	20 ng/ μL
WGBS	Genomic DNA · cells · tissue	$\geq 1 \mu\text{g} \cdot \geq 1 \times 10^6 \cdot \geq 50 \text{ mg}$	200 ng	10 ng/ μL
RRBS	Genomic DNA · cells · tissue	$\geq 1 \mu\text{g} \cdot \geq 5 \times 10^6 \cdot \geq 30 \text{ mg}$	20 ng · 3×10^3	20 ng/ μL
Targeted Bisulfite Sequencing	Genomic DNA · cells · tissue	$\geq 500 \text{ ng} \cdot \geq 1 \times 10^6 \cdot \geq 20 \text{ mg}$	50 ng	10 ng/ μL

RNA sequencing service sample requirements

RNA can be submitted in RNase-free water, RNA stabilization reagent, or 10 mM Tris pH 8.0. Total RNA should be DNA-free, with A260/A280 $\geq$ 1.8, A260/A230 $\geq$ 1.8 and **RIN** $\geq$ 6. Ship on dry ice. Long-read RNA sequencing requires **RIN** $\geq$ 8.

Concentration note. Values below assume fluorometry. Using spectrophotometry instead? Increase concentrations by roughly 2x.

RNA sequencing services

Service	Sample type	Recommended	Minimum	Min. concentration
Whole Transcriptome Sequencing	Total RNA	$\geq 3 \mu\text{g}$	1 μg	20 ng/ μL
Low-Input RNA Sequencing	Total RNA	$\geq 20 \text{ ng}$	20 pg	1 pg/ μL
mRNA Sequencing	Total RNA · cells · tissue	$\geq 500 \text{ ng} \cdot \geq 1 \times 10^6 \cdot \geq 50 \text{ mg}$	200 ng · 10 mg	20 ng/ μL
Total RNA / LncRNA Sequencing	Total RNA · cells · tissue	$\geq 2 \mu\text{g} \cdot \geq 2 \times 10^6 \cdot \geq 500 \text{ mg}$	500 ng · 100 mg	50 ng/ μL
CircRNA Sequencing	Total RNA · cells · tissue	$\geq 5 \mu\text{g} \cdot \geq 2 \times 10^6 \cdot \geq 500 \text{ mg}$	2 μg · 100 mg	50 ng/ μL
Metatranscriptome	Total RNA · cells · environmental	$\geq 4 \mu\text{g} \cdot \geq 5 \times 10^6 \cdot \geq 1.5 \text{ g}$	3 μg	50 ng/ μL
Bacterial RNA Sequencing	Total RNA · cells	$\geq 1 \mu\text{g} \cdot \geq 1 \times 10^7$	—	—
TCR-seq	Total RNA	$\geq 100 \text{ ng}$	—	10 ng/ μL
Ribo-seq	Cells · tissue	$\geq 5 \times 10^6 - 10^7 \cdot \geq 400 \text{ mg}$	200 mg	—
Dual RNA-seq	Total RNA · cells · tissue	$\geq 1 \mu\text{g} \cdot \geq 5 \times 10^6 \cdot \geq 500 \text{ mg}$	200 ng · 100 mg	10 ng/ μL
Exosomal RNA Sequencing	Total RNA · cell supernatant · serum/plasma	$\geq 100 \text{ ng} \cdot \geq 15 \text{ mL} \cdot \geq 1 \text{ mL}$	—	20 ng/ μL
Nanopore Full-Length Transcripts	Total RNA · RIN ≥ 8	$\geq 2 \mu\text{g}$	—	—
Nanopore Direct RNA Sequencing	Total RNA · RIN ≥ 8	$\geq 15 \mu\text{g}$	—	—

Single-cell and spatial genomics

Service	Sample type	Recommended quantity and quality	Minimum
ScRNA-seq	Single-cell suspension, fresh tissue	2×10^6 cells	1×10^6 cells
SnRNA-seq	Snap-frozen tissue	$\geq 100 \text{ mg}$, contact us for details	
10X Visium Spatial	OCT-embedded tissue, FFPE	6.5 mm $\times$ 6.5 mm section	
scATAC-seq	Nuclei suspension · cell suspension · fresh tissue · whole blood (EDTA)	1×10^6 , nuclei $< 40 \mu\text{m}$, $> 95\%$ intact · $\geq 1 \times 10^6$, viability $> 80\%$, 700–1200 cells/ μL · 200 mg · $\geq 5 \text{ mL}$	5×10^5

Service	Sample type	Recommended quantity and quality	Minimum
Single Cell Genome Sequencing	Cells · DNA	1–10 ³ in 1× PBS without Ca ²⁺ /Mg ²⁺ , ≤ 2 µL	≥ 0.5 pg
ScRRBS	Cell lines, primary cells, fresh tissue, frozen cells	200 µL PCR tubes, 5 µL lysate per tube, ≤ 1 µL buffer, ≥ 3 biological replicates	

The Sample Submission Form

Every shipment needs a completed Sample Submission Form, either emailed ahead or on paper with the samples. Sample names on the form must match the labels on the tubes exactly, in name and in quantity. Please also email an electronic copy of the form and any QC data you already have: concentration, OD ratios, RIN.

Tube labeling. Label the top of each tube lid with a maximum of four alphanumeric characters, for example 4B01. Write sample names with a black permanent marker at the top and side of the tube, never with an oil pen directly on the tube wall.

Shipping guidelines

A shipping address, tracking checklist and courier account details are provided once your booking is confirmed, since logistics vary by platform and lab location. The rules below apply to every shipment.

1. **Match the form to the shipment.** Double-check that sample names and quantities on the submission form exactly match what is physically sent.
2. **Use 1.5 mL centrifuge tubes** where possible, sealed with parafilm. Insert them into 50 mL centrifuge tubes, or another rigid support, padded with cotton or foam so they cannot be crushed in transit.
3. **For large-scale projects**, use well-sealed 96-well semi- or fully-skirted PCR plates, or strip-tubes with individually attached caps. Seal every well with an adhesive sheet or foil and cushion the plate in a sturdy box. Ship on frozen blue ice or dry ice so samples stay frozen throughout.
4. **Never write directly on the tube with an oil pen.** Use a black permanent marker at the top and side of each tube.
5. **DNA in 70% ethanol** can travel at room temperature. **DNA in H₂O or TE buffer** needs ice packs.
6. **RNA, cells, bacteria and frozen tissue** should be snap-frozen in liquid nitrogen, then shipped on dry ice. The amount of dry ice or ice packs needed depends on season, transit time and foam box thickness.
7. **Blood samples** travel best in 5 to 10 mL plastic anticoagulant collection vessels, each wrapped in bubble wrap and packed in a rigid box to prevent crushing.
8. **Notify us before shipping.** Send the Sample Submission Form and the tracking number by email so we can register and process your samples on arrival. We cannot receive packages at weekends, so please time shipments to arrive on a weekday.
9. **We recommend FedEx, DHL or UPS** for all shipments.

Sending raw material rather than extracted nucleic acids?

Our Sample Preparation and Sample Extraction & Quality Control platforms handle extraction and QC reporting for you. Collection and storage protocols by sample type, from blood and FFPE to saliva, swabs and stool, are at omics4.com/sampling-protocols.

Book a service

omics4.com/contact
Quote typically within 2 business days

Turnaround

72 h for catalogue services
3 to 8 weeks for a scoped project

Contact

sales@omics4.com
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