



Allegro SPET Sample preparation guidelines

IGATech offers nucleic acids extraction service and we can set up a dedicated extraction workflow for your specific substrate. Please enquire.

General best practice and quality for DNA:

- $260/280 > 1.8$ and $260/230 > 1.8$
- Quantification made by dsDNA-specific fluorimetry (Qubit/fluorimeter)
- Store the DNA in stabilizing buffer (Tris-HCl pH 8.0-8.5)
- Do not provide DNA with EDTA (conc. > 0.1 mM)
- DNA must be RNA-free (so RNase treatment is strongly suggested)
- Does not contain phenol, polyphenols

Submit 1 µg of DNA per sample normalized at about 30ng/µl. Please note that fluorimetry-based quantification (e.g. Qubit, plate-reader) assays are more accurate methods than absorbance-based methods (e.g. Nanodrop) which might overestimate the quantity.

Quality of the DNA should be $260/280 > 1.8$ and $260/230 > 1.8$.

DNA must be re-suspended in 10mM Tris-HCl pH 8.5 (standard elution buffer of most commercial column-based extraction kits); water is accepted as an alternative (**NO high concentration of EDTA must be present in the solution** – e.g. no TE 1X buffer 1mM EDTA - but consider 10mM Tris-HCl as best buffer for HMW DNA stability or 10mM Tris-HCl + 0.1 mM EDTA).

Mail DNA samples in 1.5 or 2 mL Eppendorf tubes sealed with parafilm (0.5 mL / 0.2 mL tubes will not be accepted).

If you have 24 or more samples, please put them in a 96-well skirted plate sealed with adhesive/heat-sealed aluminum foil. The tubes must have, on the vial top, a clear and permanent sign (or a thin label) with a progressive number of the mailed samples and the customer's name (at least the initials).

Send DNA samples in a cold pack (e.g. Blue ice) or dry ice. Do not ship plates without secondary containment as these may crack when placed directly on dry ice.

Please, do not forget to send us the compiled **Samples Spreadsheet**, both with the shipped parcel and via e-mail. In order to be able to properly track and safeguard your samples we also ask you to send us the **Tracking Number** via e-mail.