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Tender No: IISER/PUR/1112/MK/SB/25-26

Date: 10 Dec 2025

CORRIGENDUM RE-TENDER

Sub: Supply, Installation and commissioning of High Resolution LC-MS/MS Facility: reg

Ref: Tender Enquiry No. 2025_IISRT_880803_1

1. Since there is only one technically qualified bidder, subject to clarification of two queries, the above mentioned tender is hereby re-tendered with revised technical specifications at Annexure 1 to encourage broader participation and to enhance competitiveness: -

2. The due dates will be as follows: -

   (a) Due date: 05 Jan 2026 (1500 Hrs)
   (b) Date of opening :06 Jan 2026 (1530 Hrs)

3. All other Terms and Conditions remain the same. Bidders may quote accordingly

Thanking You,

Yours Faithfully

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10/12/25

Assistant Registrar (P&S)

Annexure 1 to Corrigendum Re-Tender No. IISER/PUR/1112/MK/SB/25-26
Dated 10 Dec 2025

Technical specifications for high-resolution LC-MS/MS facility

1. **General Requirements:**
   - A single MS/MS system should function as a high-resolution, high-mass accuracy mass spectrometer designed for clinical proteomics, quantitative proteomics, PTMs analysis, protein-protein interaction studies, top-down proteomics, targeted proteomics, single-cell proteomics, metabolomics and lipidomics.
   - It must support both Data-Dependent Acquisition (DDA) and Data-Independent Acquisition (DIA) for qualitative and quantitative analyses.
   - The instrument should be compatible with nano-LC for proteomics and UPLC for metabolomics and lipidomics, respectively.
   - The instrument must support parallel reaction monitoring (PRM) and multiple reaction monitoring (MRM) for targeted quantitative proteomics workflows.
   - The system should allow for high-throughput analysis with high sensitivity and low sample consumption.
   - Higher sensitivity measurements for low sample input (<250 picograms), including single cell proteomics applications
   - Should support both label-free quantitation (LFQ) and isobaric labeling (including TMT 6-plex or more, 4 to 8-plex iTRAQ).
   - A hands-on training should be provided by the vendor application team on the instrument operation, basic instrument maintenance and core applications level training.
   - The instrument must be optimized for short-gradient, high-throughput and low-sample input proteomics.
   - Should allow separation of co-eluting isobaric ions based on the differential mobility of ions (IM or FAIMS or equivalent should be quoted)

Mass spectrometer specifications

1. **Ionization Source**
   - Heated dual Electro-Spray Ionization (ESI/APCI) source and nanoESI with both positive and negative ionization modes.
   - Flow rate: 100 nL/min to 1000 nL/min or better, without spitting of the flow.
   - Should come along with column heating support.
2. **Mass Range:** Precursor ion m/z range of 50–4,000 or higher.
3. **Mass Resolution:** 55,000 or higher for TOF; 120,000 or higher for Orbitrap; and 80,000 or higher for Astral
   - Should be capable of resolving isobaric iTRAQ and TMT reporter ions
4. **Mass Accuracy:** < 3 ppm in both MS and MS/MS modes using internal and external calibration.

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5. Mass Analyzers: The instrument should have

- Quadrupole mass filter for selective ion isolation.
- TOF, Orbitrap, or Astral mass analyzer with ultra-fast duty cycles.

6. Scan Acquisition Rate: 200 Hz or higher for MS/MS scans.

7. Dynamic Range: At least 5 orders of linear dynamic range or better, to identify both and quantify both high and low abundant analytes in complex biological samples.

8.The system must support ion trapping (mild trapping) throughout the run

9. Fragmentation Methods

- Multiple fragmentation options, including Collision-Induced Dissociation (CID)/ Higher energy Collisional Dissociation (HCD).
- Suitable for routine peptide sequencing and analysis of post-translational modifications (PTMs).

10. Calibrant Delivery: Provision for infusion of calibrant and reference compounds.

11.Internal mass calibration: The system should support internal reference mass correction (lock mass) for both MS and MS/MS operations

12. Mass Sensitivity: Picogram-level sensitivity for standard samples such as 1 pg of reserpine with S/N ratio >500:1 in MS mode.

13. Scan mode: Must acquire and display Full Scan mass spectra (MS), Full Scan MS/MS spectra Selected Reaction Monitoring/Multiple Reaction Monitoring (SRM/MRM) like data sets (Parallel Reaction Monitoring), multiplexed SIM and multiplexed MS/MS mass spectra of up to 10 simultaneously detected precursor ions.

14. The system must allow parallel ion accumulation (MS and MS/MS) and serial fragmentation for faster acquisition.

15. UPS (Uninterruptible Power Supply)

- Online UPS with a capacity of 20 kVA or higher.
- Minimum backup of 60 minutes for the entire system (including LC unit).
- Must include necessary battery and battery rack.

16. Vacuum System

- Highly efficient turbo molecular pumps backed by rotary mechanical pumps.
- All required accessories for vacuum system operation should be included.

17. Polarity Switching

- Positive and negative mode acquisition possible within a single run.
- Accuracy: <1 ppm in MS mode and <2 ppm in MS/MS mode for 10 repeat injections (reserpine or equivalent).

18. Gas Generators

- Low-noise nitrogen gas generator (>99% purity) with inbuilt compressor and flow rate controller.
- Any additional required gases must be provided with cylinder, regulator, connectors, compressor, tubing, and filters.

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High-Performance Liquid Chromatography (HPLC) System for Proteomics

Analytical nano-LC system should be provided for solvent and sample management with the following configuration

1. Pump: High Accuracy Quaternary/Dual Pump (suitable for solvents with pH 3-10) degassing option
2. The complete LC–MS platform must be operated through a unified, single-point software control. The system should incorporate integrated leak management with safe leak handling, diagnostic tools to detect and localize leaks at nanoliter-per-minute flow rates, as well as direct flow control and automated solvent flow regulation algorithms within the operating software
3. Back Pressure Capability: 7000 psi or better. Should be compatible with analytical columns >15cm (2 µm particle size) at 300 nl/min flow rate, without any leaks in the system
4. Flow Rate: 100nL/min to 5000nL/min or greater, without flow splitting
5. Autosampler should accommodate microtiter plates or tips (96 and/ or 384 wells) with an option of active cooling or refrigerated storage for loaded samples
6. Columns and emitters: compatible with nano-scale analytical columns and capable of temperature control (ambient to ≥50 °C)
7. Design should minimize carryover between injections, with built-in options for blank runs or wash positions
8. Should be compatible with major high-resolution MS platforms (Orbitrap, TOF, and Astral), with documented successful operation
9. Must allow integration with MS acquisition software for seamless scheduling
10. The system should support automatic idle flow or wash routines to keep columns conditioned during standby.
11. Flow rates and wash solutions should be user-configurable
12. The system must include a column oven or column heater with precise temperature (upto50 °C or higher) control to ensure chromatographic stability

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Micro-flow High-Performance Liquid Chromatography (HPLC) System for Metabolomics and Lipidomics

UPLC should be suitable for both targeted and untargeted metabolomics and lipidomics workflows with robustness for continuous operation in high-throughput studies.

1. Solvent delivery system: Binary or quaternary, isocratic high-pressure gradient pumping system with high precision and low pulsation
2. Flow rate range: approximately 1 µL/min to 5 mL/min (or higher), suitable for both analytical and high-throughput workflows
3. Flow rate precision: ≤ 0.05% RSD or better
4. Pressure limit: up to 15000 psi or higher for UHPLC compatibility
5. Integrated solvent degassing system (vacuum degasser)
6. Compatible with solvents across pH 2–10 or wider
7. Autosampler: High-capacity and temperature controlled (4–40 °C) autosampler with injection volume range: nL to µL with high accuracy and precision (≤ 1% RSD)
8. Column oven with precise temperature control (ambient +10 °C to 100 °C or higher)
9. Detector Options: Multi-wavelength UV/Vis detector with diode array capability.
10. System Integration and Software
    - Single-point software control for all UHPLC modules.
    - Seamless integration with high-resolution mass spectrometry systems.
    - Support for automated sequences, data acquisition, and diagnostic functions.

Data management and software:

1. Computer workstation interfaced with LC-MS/MS system:
    - One dedicated high-performance workstation for data acquisition, interfaced directly with the mass spectrometer and LC system for real-time control and monitoring for proteomics, metabolomics and lipidomics workflows. Capable of handling large raw data files (>5 GB per run) and efficiently managing datasets from DDA, DIA, PRM, and SRM workflows. The workstation should include provisions for future software upgrades for data visualization and LC-MS/MS operation.
    - Should be provided with 20 TB (or higher) of storage
2. Separate high-end Workstation for data analysis:

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- Latest generation multi-core CPU with minimum of 16 cores
- 128 GB RAM or higher.
- 2 TB or higher SSD primary drive with additional HDD storage (8 TB or higher).
- High-resolution monitor (screen size of 27 inches or more) for data visualization
- Pre-installed with the necessary acquisition and/or analysis software provided by the vendor.
- Operating system: Windows 10 or latest version (English edition), 64 bit or better
- One laser jet black and white printer must be provided

3. Softwares:
    - Original, licensed, universal perpetual software for comprehensive control of all LC-MS frontends, including free software upgrades for 5 years
    - Latest software for bottoms-up and top-down proteomics with free upgrades for at least 3 years.
    - Should be able to analyze dataset related to DDA and DIA (library and library free) acquisitions, SILAC and reporter ions (iTRAQ/TMT) based quantitative assays, crosslinking proteomics and PTMs analysis with an option of manual configuration of new PTM masses.
    - Software for targeted and untargeted metabolomics/lipidomics analysis with both qualitative and quantitative estimations
    - Software should allow visualization of MS/MS spectra and fragment ions assignment
    - Both the systems should have the latest version of Windows and Microsoft Office
4. All hardware and software, including drivers, monitor, and device interface cards/network, must be preinstalled and preconfigured on the computer provided.
5. Crosslinking, DIA (library and library free), MS/MS spectra quality check, quantitative, SILAC, reporter ion quantitation, PTMs (configure manual), top-down, untargeted metabolomics and lipidomics

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Accessories:

1. An online UPS with a capacity of 20Kva or higher, providing a minimum backup of 60 minutes for the entire system (including the LC), should be supplied. The UPS must be accompanied by the required battery and battery rack.
2. The vendor shall supply and quote a suitable nitrogen generator. The generator must include a reliable, low-maintenance compressor with adequate capacity to deliver nitrogen of purity >99.999% for uninterrupted system operation. It should be equipped with the latest gas panel technology and a low-noise compressor design.
3. Any additional gas cylinders required for system operation shall be supplied (at least 2 quantities) by the vendor along with all necessary accessories, including regulator, gas purification panel unit, and cylinder cage/bracket. These must be installed and fitted by the vendor at no additional cost.
4. Two syringe pumps, or equivalent, shall be provided for direct sample infusion.
5. The system should be supplied with the following columns:
   - C18 25cm (or longer) x 75-150µm, <3 µm particle size: 5 analytical columns for nanoLC
   - C18 15cm x 75-150µm, <3 µm particle size: 5 analytical columns for nanoLC
   - C18 Nano-trap columns (if applicable): 5 in numbers for nano LC
   - 5 HPLC columns for metabolomics and lipidomic analysis
6. In case, trap tips such as Evotips are required, at least 10 boxes (each of 96 tips) should be quoted
7. The supply must include five emitter tips.
8. An appropriate anti-vibration table of adequate dimensions shall be provided for the LC-MS/MS platform. In the case of a floor-model mass spectrometer, one anti-vibration table should be supplied for the LC system.
9. The vendor should provide hands-on training for two IISER TVM staff members on the LC-MS/MS system at a facility with an operational mass spectrometer, for a duration of at least one week, at free of cost. All expenses related to domestic or international travel, accommodation, and associated training costs shall be borne by the vendor.
10. The vendor shall quote all necessary accessories, spare parts, consumable kits/reagents, calibration kits in 2 numbers each
11. Three years of comprehensive warranty on the entire system (UPLCs, MS, Nitrogen generator, UPS etc.) with spares, electronic boards, hardware consumables and third-party instruments.

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10/12/25

12. The vendor should issue an undertaking that the availability of spare parts for at least 10 years from the date of successful installation.
13. All technical data sheets should be available on the vendor's public website.
14. IISER TVM will provide space with electricity and air-conditioning connections. It shall be the vendor's responsibility to install the instrument, accessories, and all necessary infrastructure and facilities required for its operation. This may include, but is not limited to, platforms, plumbing, wiring, gas cylinders and piping, gas generators, computer hardware and software installations, additional electrical wiring, switches, and any other requirements to bring the instrument to the performance qualification (PQ) level.
15. Comprehensive instrument operation and data analysis training at IISER TVM shall be provided at least twice a year for a period of five years. The supplier shall also offer training and troubleshooting support for workflow operation as needed throughout the contract period.

Optional:

1. An additional comprehensive maintenance and service contract (CMC) of 3 years for the entire system, including third-party components, offline systems, and all OEM items.
2. An extended Annual Maintenance Contract (AMC) for a further 4 years.
3. HDX accessory or module compatible with the LC-MS/MS system, suitable for performing hydrogen-deuterium exchange experiments for protein structural and interaction studies.
    - Dedicated software support for HDX data acquisition and analysis must be provided such as, including peptide mapping, differential deuterium uptake quantitation
    - A separate nanoLC for HDX module should be provided, if needed
4. Extended 5-year free upgrades for analysis software modules for proteomics, metabolomics, and lipidomics data.
5. Additional 10 boxes of trap tips, 5 analytical columns (C18, ≥25 cm length × 75 μm ID, particle size <3 μm), and 10C18 Nano-trap columns, if applicable.
6. A fully trained, qualified in-house technician, dedicated to IISER Thiruvananthapuram, for a period of 2 years to ensure smooth operation and proper maintenance of the LC-MS/MS system.
7. A vacuum centrifuge (SpeedVac or equivalent) suitable for evaporating solvents from small volumes of biological or chemical samples prior to LC-MS/MS analysis.

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