

Komaba Analysis Core

[Open Core Facility for Materials Characterization]

Komaba Analysis Core, Institute of Industrial Science

User Facilities for all scientists in private company, research institute, and University.

Komaba Analysis Core

<https://sites.google.com/g.ecc.u-tokyo.ac.jp/iis-materials-core>

What is “Komaba Analysis Core (駒場分析コア)”?

The Komaba Analysis Core has been established in FY2021. New instruments, focused ion beam microscopy (FIB-SEM), confocal microscope, cell sorter, and mass spectrometer, have been installed under a supports from the University of Tokyo Venture Ecosystem (uTIE). The aim of us is accelerations of venture business and scientific research!!

We would contribute to the development of academic researches and the creation of innovation in venture businesses by supporting research organizations inside and outside the university and private companies (especially venture businesses) through the open facilities.

How to use?

1. Submit an application form according to the application procedure
2. Technical consultation with the person in charge of each equipment and related researchers
3. Make a reservation for the equipment through the equipment manager
4. Training and/or use of the equipment
5. Payment



東京大学生産技術研究所

駒場分析コア

Go to the Official homepage!



We are always available for consultation regarding analysis and details of each instrument.

FIB-SEM

Thermo fisher Scios2



EDS (2021.12~)

TEM sample preparation and microfabrication by FIB
Observation by FE-SEM; elemental composition determination by EDS
Dark-field and bright-field image observation by STEM mode
3D multi-modal observation by FIB+SEM

Confocal microscope

Nikon Biopipeline LIVE



Confocal microscopy
Live Imaging
High Content Cell Analysis

Cell sorter

BD FACS Melody



Cell Preparation and Analysis
Plate Sorting
Simple and easy operation

Mass spectrometer

JEOL SpiralTOF-plus



Molecular weight measurement (incl. molecular weight distribution of macromolecules, host-guest complexes)
Elemental composition analysis by HR-MS
Peptide sequencing by MS/MS measurements

