The mission of the Macromolecular Structure Core is to empower users with state-of-the-art equipment and expertise to conduct structural biology research.

The MSC combines resources in two UAB facilities: the cryo-electron microscopy facility (CEMF) and the X-ray crystallography core facility (XCCF).

**CRYO-ELECTRON MICROSCOPY**

- Terje Dokland  
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**X-RAY CRYystallography**

- Champion Deivanayagam  
  Director  
  champy@uab.edu

- Norbert Schormann  
  Manager  
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- Located at CBSE 100 1025 18th Street S  
  Birmingham, AL 35294-4400
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CRYO-EM EQUIPMENT

FEI Tecnai F20
- 200 kV FEG instrument with Gatan cryo-holders
- Equipped with a Gatan K3 direct electron detector
- Used for room temperature (negative stain) and cryogenic imaging of proteins, viruses, cells etc.
- Capable of generating <4 Å resolution data

Thermo Fisher Glacios (arriving Spring 2022)
- 200 kV FEG instrument with 12-sample autoloader
- Equipped with a Falcon 3EC direct electron detector
- Routinely capable of <4 Å resolution, <2-3 Å in ideal cases
- Sample autoloader allows rapid sample throughput
- Can be fully automated for 24/7 data collection
CRYO-EM SERVICES

• Sample Preparation
  • Preparation of negatively stained samples
  • Cryogenic sample preparation using FEI Vitrobot or Gatan CryoPlunge. A variety of sample substrates are available: continuous carbon, holey carbon (1.2 to 2 μm hole size), lacey carbon, holey gold films (UltrAuFoil)

• Cryo-EM and Room Temperature Imaging
  • Observation of proteins and protein complexes larger than ~100 kDa, viruses, liposomes and other lipid-containing samples, intact prokaryotic cells up to ~1 μm thick by cryo-EM and negative stain

• Data Processing and 3D Reconstruction
  • Data pre-processing, particle picking, 2D and 3D classification and refinement with RELION, EMAN and other software
  • Generation of 3D structures of single proteins, protein complexes

• Electron Tomography
  • Tomographic data collection and processing
**High throughput protein crystallization and optimization**

The High throughput (HTP) facility is capable of routinely performing thousands of protein only and co-crystallization experiments in nanoliter volumes for both membrane and aqueous proteins. Our HTP robots include (a) Art Robbins Gryphon LCP System (Room temp) and (b) Rigaku Phoenix RE System (4°C) (c) Formulatrix crystal imaging systems with UV imaging technology.

**X-ray diffraction and analysis**

Our state-of-the-art equipment includes the Micromax 007HF generator outfitted with Osmic HF (left) and HR (right) optics. On the left side is the Dectris Pilatus 200k mounted on a four-circle goniometer. On the right side we have the Raxis IV++ image plate detector mounted on an inverted phi. The core-facility also offers service crystallography lending expertise in crystallizing, collecting, analyzing, resolving and submitting structures to PDB and helping with publications.

Please contact nschorm@uab.edu for further details.

www.uab.edu/xray
**Mission:** To provide investigators state-of-the-art instrumentation and resources to carry out structural biology studies.

**UAB is a member of the Southeast Regional Collaborative Access Team (SER-CAT) that provides UAB researchers access to two of the most powerful beam lines at the Argonne National Laboratory for high-resolution structural analyses, drug design, protein engineering and site-directed mutagenesis projects.**

For further details please contact:
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Biophysical characterization of proteins

Monolith - X

Auto ITC200

Prometheus Nano DSF

Olis CD spectroscope

Cap DSC

PTI Fluorescence Detector

The core facility has numerous state-of-the-art equipments to biophysically characterize proteins and their interactions. These include (i) Monolith X, (ii) Auto ITC 200, (iii) Prometheus Nano DSF, (iv) Olis CD Spectrophotometer, (v) Cap DSC and (vi) PTI Fluorescence Detector.

For details, please contact Wendy Yang (yangzw@uab.edu).

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