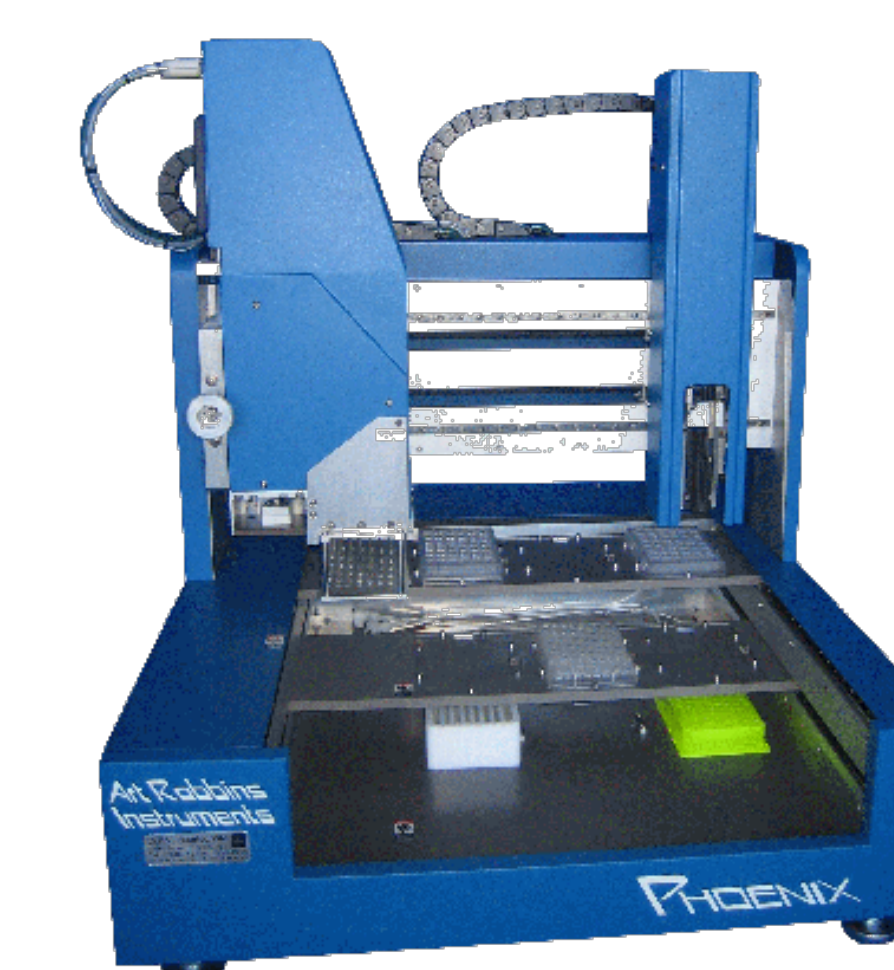


Do you want diffraction quality crystals of your protein?

You need High Throughput Nano-crystallization We can perform thousands of native and co-crystallization within nano-liter volumes of both membrane and aqueous proteins.

- Ability to screen detergent & lipid based conditions
- Crystallization systems (Art Robbins Phoenix and Gryphon LCP)
- New Formulatrix crystal Imaging system with UV imaging technology
- SONICC (Second order non-linear imaging of Chiral Crystals) for detection of sub micron crystals.



Do you want the three dimensional structure of your protein?

You need X-ray diffraction and access to National Synchrotron Radiation facility: We can obtain single crystal X-ray diffraction data from crystals for high-resolution structural analysis, drug design, protein engineering, site-directed mutagenesis projects.

- Access to In-house X-ray facility for immediate analysis with Rigaku Micromax007HF rotating anode with a micro focus beam and new Pilatus 200k detector and Raxis IV++ image plate detector.
- Access to high powered synchrotron in Chicago through our membership in the Southeast Regional Collaborative Access Team (SER-CAT).



Do you want know if your protein is properly folded and thermally stable?

You need Differential Scanning Calorimetry: Automated Differential Scanning Calorimetry (DSC) can measure the heat absorbed during macromolecular unfolding thereby providing the information on the thermodynamic stability of the molecule.

- Determine if the protein is properly or completely folded.
- Identify presence of domains and extent of interactions between different domains
- Provides insights into affects of ligands and binding partners on the stability and the structure of the molecule.



Do you want information about your protein interacting with a ligand or peptide/small molecule compound?

You need Differential Scanning Calorimetry: Automated Isothermal Titrations Calorimetry (ITC) determines the binding by small molecules, proteins, peptides, antibodies, nucleic acids, lipids and other bio molecules.

- ITC enables the determination of all binding parameters including stoichiometry in a single experiment, label-free an without need for immobilization.



Are you looking to detect and quantify binding kinetics?

You need BIAcore:

BIAcore2000 can be used to detect and quantify the binding kinetics between interacting partners in real time.

- Allows determination of equilibrium binding constants
- No labeling of either binding partner is necessary
- Microgram quantities of sample, and high purity not essential.



Do you want information about NMR or Cryo-Electron Microscopy

For NMR Contact Dr. Rama Krishna (nrk@uab.edu)

For Cryo-Electron Microscopy contact Dr. Terje Dokland (Dokland@uab.edu)

View their respective Core day posters.