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 nanoliter 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.

Contact: Dr. Deivanayagam, champy@uab.edu