



Nationwide Voucher Program

Purpose: The IDeA National Resource for Quantitative Proteomics provides subsidized access to sophisticated proteomics services for investigators performing biomedical research within the mission of NIGMS (<http://idearesourceproteomics.org/>). In addition to providing cost effective access to a variety of proteomics services, the resource supports a competitive voucher program that provides fully subsidized access at no cost to the user. The goal of the voucher program is to provide pilot scale data to investigators that will create new hypotheses, support publications, and support on-going research studies within the mission of NIGMS. This voucher program supports discovery proteomics workflows limited to 10 sample Tandem Mass Tag (TMT) or 20 sample data independent acquisition (DIA) quantitative proteomic platforms. For example, a 10-plex TMT could be 5 biological replicates of a control versus 5 biological replicates of a treated cell line, while a 20 sample DIA could be 10 control vs 10 experimental tissue/plasma samples. Interested applicants may contact the resource prior to applying to discuss the proposed sample analysis and determine eligibility for the voucher program.

Voucher application due dates: 5:00pm on October 15, February 15, June 15

Earliest start date: November 1, March 1, July 1

Anticipated number of awards: 100 annually

Award budget: Fee-free voucher for 10-plex TMT (>7,000 proteins) or 20 sample DIA

Award Period: Samples must be submitted within 4 months from award date

Eligibility: One awarded voucher per laboratory Principal Investigator per year. Priority will be given to researchers funded by NIGMS, funded through the NIGMS-IDeA Program, and early-stage/new investigators working within the mission of NIGMS. Only one submission per laboratory Principal Investigator per due date.

Pre-submission consultation: Interested applicants may contact the resource at IDeAproteomics@uams.edu to discuss the proposed sample analysis and determine voucher eligibility.

Content and form of application submission: Applications are limited to 2 pages (11pt font, single spaced, 0.5 inch margins) and should include the following sections: *Project Overview* (outlining the specific research question), *Preliminary Studies* (providing example data to support the proposed proteomics analysis), *Quality Control Data* (provide evidence of sample quality such as a gel image, verification of 50 micrograms of protein or 25 microliters of plasma/serum, and details on sample homogenization including buffer components), and *Data Utilization* (discussing how the proteomics data will be used to support work within the scope of NIGMS). An optional pre-submission consultation may be used to determine whether TMT or DIA proteomics would be most appropriate for the study. Applications are to be submitted as a PDF file at <https://is.gd/IDeAVoucher>.

Other documents for submission: Principal Investigator NIH Biosketch and NIH Other Support documents.

Other requirements: For eligibility, recipients will be required to participate in pre- and post-award surveys.

Contacts: For general questions, contact IDeAproteomics@uams.edu. For administrative questions, contact Ms. Sonet Weed (SWeed@uams.edu)