**Facilities and Resources:** Coronavirus-related resources

Biosafety Lab 3 Facility: Biohazards: We will use the virulent XXX for this work. Manipulation of XXXwill be performed in the University of Rochester BSL3 facility with the rules and protocols set forth in the UR BSL-3 Program Manual as approved by the UR Institutional Biosafety Committee and the UR BSL3 User Group. The UR BSL3 facility is in good standing with University of Rochester's department of Environmental Health and Safety. The PI’s main laboratory at the University of Rochester is a BSL2 laboratory, in good standing with the Institutional Biosafety Committee and the University of Rochester's department of Environmental Health and Safety. All lab members are trained in laboratory safety, and BSL2 (and BSL3, as needed) procedures, with yearly refresher training. UR Biosafety Level 3 (BSL3) Facility: The UR BSL3 Facility has been operational since 2000. It has a clean anteroom and an inner containment lab. The inner lab has four class II biohazard hoods, a pass-through autoclave, dunk tank, air and CO2 incubators, a centrifuge with swinging bucket, highspeed, and microcentrifuge rotors, an inverted microscope, an electroporator, a cup horn sonicator, a FastPrep lysis machine, a spectrophotometer, a refrigerator, two -80°C freezers, a liquid nitrogen storage unit, and safety equipment. The BSL-3 facility is located in the Kornberg Medical Research Building, which is separate from, but connected to, the Delmonte Building where XXXX laboratory is located.

University Inventory of cornonavirus-related reagents: The University of Rochester has collected an inventory of cell lines, viruses, reagent, etc. that might be useful to coronavirus-related research.

Remote consent of human subjects: The University of Rochester Office of Human Subject Protection has a remote consent policy (http://www.rochester.edu/ohsp/documents/ohsp/pdf/policiesAndGuidance/Guideline\_REDCap\_eConsent.pdf). This policy outlines the methods for getting remote consent approved for a research study. The University uses the REDCap platform for remote consenting and how that platform will be used is also addressed in the policy.

The CTSI Informatics Teamhelps investigators:1) Think about and organize measures and data; 2) Create systems to capture data; 3) Wrangle existing data into new datasets; 4) Create protocols, systems, and policies for managing data resources; and 5) Interface technical, scientific, analytic, and access dimensions. The following resources are available in the CTSI Informatics program:

* TriNetX- software tools to query electronic health record for patient/cohort discovery for study feasibility based upon clinical characteristics, such as COVID-19 positive patients. TriNetX at URMC serves as the primary patient cohort discovery tool, providing powerful and intuitive query building functions that allow investigators to query EMR data in a completely self-serviceable and secure way to obtain summary patient counts. Investigators can explore a Limited Dataset extraction of Electronic Health Record (EHR) data of UR Medicine for over 1.5 million patients in support of either patient cohort discovery for preparatory to research or trial feasibility assessment. Once a patient cohort is identified, investigators can work with CTSI Informatics Service team to obtain patient-level data via the data governance process vetted by Research Subjects Review Board (RSRB) and Privacy Office at URMC.
* Clinical Data Request Service - CTSI has an established Electronic Health Record (EHR) data extraction service in compliance with URMC Research Subjects Review Board (RSRB) and Privacy Office. Research Informaticians work with investigators and URMC Clinical IT to define EHR dataset requirements. CTSI Informatics Service team can also server as Honest Broker if a de-identified dataset is required.
* REDCap - an online research data capture and management tool
* BLIS: comprehensive clinical, specimen and assay data management system (see below)
* Biospecimen inventory data management BSI® - CTSI Informatics can provide specimen inventory management software, including vial label generation, and vial location (box, shelf, freeze) information.

Bio-Lab Informatics Server (BLIS) is a comprehensive, web-based data management system developed to store, integrate, analyze, and securely share biomedical research data. BLIS is built using the open-source LabKey Server that provides a number of experiment modules for managing laboratory assay workflows and flexible architecture for customization. The BLIS study module serves as a data portal to integrate clinical, specimen and laboratory results. A CTSI Informatics team comprised of professional software developers, bioinformaticians and biostatisticians extend the BLIS system to meet specific project and assay workflow requirements. We partner with Genomics Research Center and the Center for Integrated Research Computing to implement workflows for managing transcriptomics and microbiome data. Experiment and multi-step workflow modules currently available for: Flow Cytometry, Luminex®, ELISpot, ELISA, Nab, TaqMan Array Card® (rtPCR), Bioanalyzer, Illumina sequencing (HiSeq, MiSeq), Proteomics, Histology Imaging. Additional BLIS features include: Charting tools enable users to create their own data plots and charts without needing to leave BLIS; Integrates with REDCap and other applications for clinical data capture; Integrates specimen inventory records (BSI, spreadsheets to track specimens and metadata, and create shipping requests and manifests; Application Programming Interface (API) to query data for analysis in external tools and languages including R, SAS, Python, Perl, and Java; Robust and flexible role and group based access controls; User-defined wiki pages to support research team collaboration; Issue trackers for data and workflow discrepancies and remediation; HIPAA and FISMA compliant. BLIS is available through a combination of institutional support and extramural funding.

The CTSI provides consultations to help research teams plan informatics-related projects, and collaborates with teams to make use of biomedical informatics methods and resources to facilitate and expand the scope of their work. Available consultation types include:

* Data management: plan approaches to capture, organize and transform data to support research needs
* REDCap: determine if REDCap is the right tool for your data capture needs and help you get started
* Clinical data access: make plans to acquire the clinical data you need for your research project
* Community and population health data: assess data and informatics needs for community-based or population health research projects
* Federal public use data access: access and analyze public access datasets from the CDC and other federal agencies, including the National Health and Nutrition Examination Survey (NHANES), the National Health Care Surveys, The National Vital Statistics System (NVSS), the National Survey of Family Growth (NSFG), the National Health Interview Survey (NHIS), the National Immunization Survey (NIS), Longitudinal Studies of Aging (LSOA), the State and Local Integrated Telephone Survey (SLAITS) and the Behavioral Risk Factor Surveillance System (BRFSS)
* Clinical systems in research: make plans to utilize eRecord and other clinical systems to support your research project
* IT systems in research: get advice regarding innovative information technology, systems and tools, or related methods, to support your research projects
* Bioinformatics analysis: make plans to develop or apply analytic and statistical methods to biological data

Clinical testing for virus by RT-PCR

The Clinical Pathology laboratory has the following COVID testing platforms: the Roche 8800, Cepheid, and Focus (Diasorin) platforms.

Antibody Testing:

The Laboratory of Dr. Benjamin Miller has developed a multiplex, quantitative, label-free antigen array for detection of antibodies to coronavirus antigens. Built on the Arrayed Imaging Reflectometry (AIR) platform, the 11-plex array includes 9 coronavirus antigens including SARS-CoV2: spike protein S1, S2, RBD, and S1+S2 extracellular domains; SARS-CoV1 spike protein S1+S2 extracellular domain, MERS spike protein RBD, and HuCoV HKU isolate spike protein S1+S2 extracellular domain. On-chip positive and negative controls for human IgG and IgM are also included on the array. Array development has focused on human serum, but plasma is also amenable to this technique. Fingerstick quantities of blood are sufficient for a single chip measurement. Because the assay is label-free, no secondary antibody or other labeling step is required.

In order to quantify the breadth of the anti-SARS2 IgG mediated immunity, Dr. Martin Zand (PI) and Dr. Jiong Wang (co-Investigator) have developed the mPLEX-CoV assay a multiplex method that simultaneously measures absolute antibody concentrations (IgG, IgM or IgA) against surface spike (S) and nucleocapsid (N) proteins from 8 CoV strains (SARS1, SARS2, OC43, HKU1, NL63, OC43, RaTG, MERS). This assay is based on our prior work with influenza, where we developed the mPLEX-Flu assay, which is able to measure anti-HA protein IgG/IgA/IgM simultaneously in up to 50 influenza strains.3, 4, 6, 11 We have previously demonstrated that the mPLEX-Flu assay has several advantages over ELISA, point of care lateral flow, and protein microarray assays, including: a linear readout over 4 logs,11 5-10µl sample sizes permit- ting either traditional serum from phlebotomy or volumentric microsampling using fingerstick blood technology,12 extremely low inter- and intra- assay variance with improved specificity and sensitivity over titering assays such as ELISA.3, 4 The mPLEX-Flu assay can measure IgM, IgG and IgA in serum, plasma, nasal washings, breast milk, and cell culture supernatants.5, 7, 11, 12 The mPLEX-CoV assay uses the exact same system, with trimerized, recombinant CoV spike (rS) and nucelocapsid (rN) proteins expressed in a baculovirus system, isolated un- der non-denaturing conditions, and covalently linked to fluorescently bar-coded micro beads. We have expressed proteins from 8 coronavirus strains, including the commonly circulating CoV strains,66 and are rapidly work- ing to express new variants of SARS2 S- and N- proteins as sequences are published. The mean fluorescence intensities (MFI) can be translated into an Ig concentration (ng/ml) for each S- or N- CoV protein using a standard curve.

Institutional Excellence in Infectious Disease Research: We have a strong individual and team-based clinical and translational research programs in vaccines, human immunology and infectious diseases. These programs have matured and risen in sophistication, commanding over $10M in annual NIH funding. The University of Rochester is home to one five national Centers of Excellence in Influenza Research and Surveillance, and we house one of 9 national Vaccines and Treatments Evaluation Units (VTEU) as part of the Infectious Disease Research Consortium. These programs are founded upon and depend on collaborative relationships between basic and clinical research faculty. Rochester is well positioned for playing a key role in the development, testing, and analysis of novel therapeutics and vaccines, and to study the natural history and pathogenesis of seasonal and emerging infections, including the SARS-CoV-2. Infectious diseases cut across virtually all areas of medicine- aging, immunodeficiency, cancer, transplant, orthopedics, eye, gut, skin, autoimmunity, neonatology, and public health. There are opportunities for human behavior and behavior modification, cognition, anthropology, ethics, and history to innovate strategies for better control of infectious diseases as well as leadership in team research. The use of Big Data in immunology & infectious disease is increasing rapidly, offering opportunities for application development for data science students and faculty within GIDS. Advances in optics and imaging are fueling innovation in infectious disease and immunology research.