CMA use only

#Samples: ________

#48h Priority: ____ **#MS^n**_________

#Protein ID: ____ **#Prep:** _______

Receive date: ___________ **by** _______

Analysis date: ___________ **by** _______

Notebook/Page #: _________________

CORONAVIRUS-19 SDO V1.0

Mass Spectrometry Sample Submission Form

Dr. Mark E. Bier, Director
Center for Molecular Analysis
Dept. of Chemistry
Mellon Institute Bldg
Carnegie Mellon University
4400 Fifth Avenue
Pittsburgh, PA 15213

http://www.chem.cmu.edu/cma/
mbier@andrew.cmu.edu
412-268-3540 (O)
412-268-7548 (LAB)

I. Billing Information:

CHARGE NUMBER (Oracle (CMU) OR PO (non-CMU) #): ____

Name: ______________________________ **Date:** ____________ **Email:** _________________________________

Phone: _____________________________ **Faculty Advisor / PI:** _______________________________

Department / Room: ____

Billing address (non-CMU): ____

II. Sample Preparation:

Guidelines: https://www.cmu.edu/chemistry/facilities/cma/instrument/mass_spec.html *Additional rates may apply if not followed.*

- Submit this SDO form by email to: ldugan@andrew.cmu.edu and copy to mbier@cmu.edu.
- **FOR ESI MS:** Label all sample vials using a laminated label with your name, date and complete sample contents.
- **FOR MALDI MS:** Spot your samples onto your MALDI PLATE with a standard, place plate in a sterile plastic container and note the well information on this sheet.
- See the special coronavirus drop-off instruction of the back of this form.

III. Sample Information:

[ ] Not toxic [ ] Unknown [ ] Toxic (explain): ____

Concentration: ________________ **Solvent system:** ________________________________ **purity:** _________**%**

Compatible solvents: _____________________________ **Volume of sample:** ____________________________

Counter ions, salts, and buffers in solution (include conc.): ____________________________________

Isotopic enrichment? ________________ **Storage Temperature: [ ] RT [ ] 2-8ºC [ ] -20°C**

Special handling: ____ **Light sensitive? [ ] No [ ] Yes**

Molecular Formula: _____________________________ **MW** ____________________ **[ ] Avg. or [ ] Monoisotopic**

Brief description of the project: ____

Masses / mass range of interest: ____

IV. Analysis Information:

Analysis priority: **[ ] Standard (1 week)** **[ ] Priority (48 hrs. – double rate)**

Ionization type: **[ ] ESI** **[ ] MALDI** **[ ] APCI**

Scans required: **[ ] (+) Mode** **[ ] (-) Mode** **[ ] MS/MS of masses:**___________________

Additional options: **[ ] High Resolution MS** **[ ] Protein identification (double rate)**

Additional rates may apply **[ ] Deconvolution** **[ ] LC-MS** **[ ] Polymeric analysis ($M_{n,w,z}$ and PDI)**

EMAIL RESULTS: **[ ] PowerPoint** **[ ] RAW DATA FORMAT**

V. Attach previous data, chemical structures, or other information to this sheet.

CORONAVIRUS-19 SDO V1.0

SAMPLE DROP-OFF PROCEDURE (SDO): (Addendum to Pandemic Safety and Preparedness Plan)

The Center for Molecular Analysis will operate under a Sample Drop-off (SDO) mode for all mass spectrometry samples until the pandemic is over. The following procedure will be used for SDOs:

Sample submission Form:

Send a sample submission form by email to the TA, Liam Dugan, ldugan@andrew.cmu.edu and copy to Mark Bier at, mbier@andrew.cmu.edu for each sample set. Paper submission will not be accepted. Samples will not be run without a completed form. For the form please see: https://www.cmu.edu/chemistry/facilities/cma/sample.html. This webpage will be updated with the new COVID-19 SDO procedures.

Sample decontamination:

All samples must be decontaminated by submitter prior to drop-off with 70% alcohol. The labels must be able to withstand this decontamination treatment so that the printed information is not lost.

Sample Drop-off (SDO)

1. The SDO area is located is outside of MI551 at the entrance to the CMA. This horizontal space for samples has been placed at least six feet from the door to MI551. The space is labelled for 'sample drop-off' and 'post-analysis sample pick-up'. Pick-up of unused samples must occur within one week of the receipt of data or they will be disposed.

2. Drop-off samples outside the door to MI551 with properly labeled vials with the contents, name and date using a laminated labeler. Brother Corporation offers such labelers. (For example, Brother P-touch, PTD210). Labels must withstand a spray of 70% alcohol.

3. The CMA TA will pick-up the samples from outside MI551 and further decontaminate them after receipt of an email from the submitter that includes the sample submission form. A hardcopy of the sample submission form should **not** be left with the sample.

4. Samples from other non-CMU labs should mail the samples to the Center with attention to Mark Bier at the following address:

   Mark Bier, Director
   SDO
   Center for Molecular Analysis
   Carnegie Mellon University
   4400 Fifth Ave
   Pittsburgh, PA 15213

5. For some non-CMU samples, an exception to shipping samples can be made by the director. Bier Lab members may then receive samples from other laboratories outside of the Mellon Institute building at a pre-determined drop-spot. This has been done since April 2020 for the collaborative Pitt/UPMC COVID-19 vaccine project.

Data Results

Data results will be sent electronically by email to the submitter in the form of a Microsoft PowerPoint doc or raw data files or both.

Data Consultations: Any data discussion will be done by phone, ZOOM mtg or email.