University of North Carolina at Chapel Hill

Michael Hooker Proteomics Core

Form associated with:
Service Project MHPC-TG-1105 at Michael Hooker Proteomics Core
Owner: Thomas Gilbert (Willson, Tim (UNC-CH) Lab)

LC-MS/MS Analysis - Sample Submission

* **Date:** June 17, 2022 16:19

* **Name:** Karim Gilbert

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* **PI name:** Tim Wilson/Lee Graves

* **PI email address:** lmg@med.unc.edu

* **Institution:** UNC

* **Department:** Pharmacology

* **Prior to submitting this iLab request, have you discussed your project with the Proteomics Core Staff (email/meeting)?**
  ⦿ yes
  ○ no

* **Project name:**
  Characterization of Putative Kinase Inhibitors as anti MRSA agents

* **Describe the purpose of this project:**
  The purpose of this project is to identify potential kinase targets of novel developed by the SGC. These compounds have shown potential as anti-MRSA agents and the investigators are looking to characterize the activity of the compounds. This is a repeat of a pervious experiment

  Fill out the sample information form below to the best of your ability.
  The physical sample tubes should, at minimum, be labeled with the sample number below as listed on the form. Additional sample name on the sample tube is helpful (IF legible). Please include sample name and replicate number. For sample group ID, here is an example: if you have listed 'IgG IP, rep1' as the sample name, the sample group ID would be 'control'.

* **Sample Information Form**

	Sample Name	Sample Group ID	Biological Source	Expression Host (species)	Est. Concentration (ug/ul)	Sample Volume (ul)	Sample type (in-gel/in-solution/on-bead)
1	DMSO	Cell line	Human	5 mg starting material	n/a	Dry	
2	ALMDAI-26 0.01uM	Cell line	Human	5 mg starting material	n/a	Dry	
3	ALMDAI 26 0.1uM	Cell line	Human	5 mg starting material	n/a	Dry	
4	ALMDAI 26 1uM	Cell line	Human	5 mg starting material	n/a	Dry	

	Sample Name	Sample Group ID	Biological Source	Expression Host (species)	Est. Concentration (ug/ul)	Sample Volume (ul)	Sample type (in-gel/in-solution/on-bead)
5	ALMDAI 28 0.01uM	Cell line	Human	5 mg starting material	n/a	Dry	
6	ALMDAI 28 0.1uM	Cell line	Human	5 mg starting material	n/a	Dry	
7	ALMDAI 28 1uM	Cell line	Human	5 mg starting material	n/a	Dry	
8	Dinaciclib 0.01uM	Cell line	Human	5 mg starting material	n/a	Dry	
9	Dinaciclib 0.1uM	Cell line	Human	5 mg starting material	n/a	Dry	
10	Dinaciclib 1uM	Cell line	Human	5 mg starting material	n/a	Dry	
11							

* **Briefly outline sample preparation steps you followed (including specific buffers used):**
Competition MIBs as described previously.

* **For in-solution or on-bead samples, buffer composition:**
N/A

For in-gel samples, please upload an annotated gel image:

If your sample information table includes samples from different conditions, please list these out. For example if you have listed "IgG" the condition name would be 'control'

For in-gel samples, do you want to pick up your gel container post-analysis?
☐ yes
☐ no

* **Type of analysis (check one):**
☐ PTM site mapping on single protein
☐ Protein characterization
☐ Proteomic profiling
☐ Phosphoproteomic profiling
☐ PTM peptide-based pulldown (acetyl/methyl/ubiqiutin)
☐ Affinity purification-mass spec (AP-MS) analysis
☑ MIB-MS kinome profiling
☐ Targeted analysis
☐ Other (specify in description)

* **Provide protein amino acid sequence (with tags) or Uniprot Accession #, specifically for: PTM site mapping, protein characterization or AP-MS projects:**
n/a

* **List any specific data analysis requests. For example: list specific software and/or data format preferences. For quantitation, list what sample group comparisons you want us to make:**
n/a

* **If this is a continuation of another project, list the project ID PC#:**
n/a

* **List any deadlines that we need to keep in mind:**
n/a