PRG 2019 DIA Study Survey

Participant matrix information

please enter the anonymous identification number you were given through email

1. Identification number

*** 2. Experience in setting up LCMSMS runs**

- ○ never set up myself
- ○ 0-2 years
- ○ 3-5 years
- ○ 6-9 years
- ○ >10 years

*** 3. Experience with DIA**

- ○ Heard about it
- ○ Tried it once
- ○ Have done it a couple of times
- ○ Expert. You should pay me to do this

Data acquisition

HPLC and MS conditions

4. Sample dissolution

Dissolution buffer

volume (uL)

Volume loaded (uL)

5. Sample loading

6. Trapping conditions (skip if trap not used)

Trap chemistry

Trap dimension (ID x length)

Trapping Solvent

Trapping time (min)

particle size (um)

pore size (A)

7. Did you use the HPLC gradient suggested

8. HPLC method

Chemistry (C18, HILIC, etc.)

Length (mm)

ID (mm)

Particle size (um)

Pore size (A)

Temperature (degree Celsius or uncontrolled)

Commercial or self packed

Flow rate (nL/min)

Gradient time (min)

Run time (min/injection)

Total instrument time spent on this study (hr)

9. Did you use provided MS method?

10. Mass Spectrometry

Mass spectrometer vendor/model

Calibration (with or without lockmass)

MS1 resolution

MS2 resolution

Fragmentation (eg. CID, HCD, ETD, etc.)

MS2 window size (m/z)

MS2 window overlap (m/z) (0 for non-overlapping windows)

cycle time (sec)

Data analysis (optional)

This entire page is optional. We would like to know how you feel about DIA data analysis. But only if you feel like sharing. Feel free to skip questions on this page.

11. Did you analyze your data

- ○ Yes - Please provide answer to questions below as available
- ○ No - Finish by clicking on "Done"

12. What software(s) did you use

13. What software is your reported results from?

14. # proteins groups identified across all runs

15. Identify the samples as blank, low spike and high spike

	blank	low spike	high spike
Sample 1	○	○	○
Sample 2	○	○	○
Sample 3	○	○	○

16. # proteins with CV <20%

Sample 1

Sample 2

Sample 3

17. %CV for the 4 spike-in proteins

Sample 1, ABRF-1

Sample 1, ABRF-2

Sample 1, ABRF-3

Sample 1, ABRF-4

Sample 2, ABRF-1

Sample 2, ABRF-2

Sample 2, ABRF-3

Sample 2, ABRF-4

Sample 3, ABRF-1

Sample 3, ABRF-2

Sample 3, ABRF-3

Sample 3, ABRF-4