13/12/2023

Minutes of the pre-Bid meeting for the supply of triple quadruple mass spectrometry setup for targeted and untargeted proteomics, metabolomics, and lipidomics

All the concerns indicated by Agilent Technologies against the published specifications were discussed in the pre-Bid meeting in presence of representatives from Agilent and Sciex. Summarized below:

Sl.No	Chapter	Specification	Requirements	Agilent Suggestions	CCMB - remarks
1	4.2.0		Untargeted	Untargeted applications are usually performed on High resolution instruments. Quadrupole based instrument are not the best suited for these applications	Untargeted applications are possible to perform with QQQ instruments. No change
2	4.2.5	Mass Resolution	The system should be capable to perform a high resolution scan where at least resolution up to 9000 (FWHM) can be achieved. This is required to resolve the isotopic peaks of the multiple charged peptides/lipids.	This cannot be done by quadrupole based instruments. Mostly it is done on TOF or trap based instruments.	Accurate molecular weight and charge state determination of analytes is an important requirement which is only possible at a high resolution. This is a application requirement. No change
3	4.2.6	Sensitivity	APCI source in positive ionization mode, for 10 pg/uL, 5 uL fixed loop injection of a standard compound on the column, the instrument must have S/N > 2,00,000:1 or better.	Please remove this because it is not available in the specsheet of all vendors.	APCI source is required for analysis of semi-polar compounds such as hormones, steroids, lipids, vitamins etc. No change
		IDL – Positive mode ESI, IDL - negative Mode ESI	positive ESI Reserpine 1 fg on column (609/195) < 0.3 fg, negative ESI Chloramphenicol 1 fg on column (321/153) < 0.3 fg	Please change to 0.4fg since 0.3 is not mentioned on our specsheet. However the specs asked can be achieved on our system if lab generated data is allowed.	changed to 0.4fg

4	4.2.8	Source Ionization Technology	3000 µL/min	Please change to 2500 ul or higher since in LCMS applications usually run on 400-800 ul max. with UHPLC front end.	changed to 2500 ul or higher
5	4.2.11	Ion polarity Mode	Polarity switching time <5 msec	Request to change Polarity Switching to 25 msec or better. THis will not impact any application in any way.	changed to 25 msec or better
6	4.2.13	MSn	At least MS3	Please note that this feature is unique to only one vendor and that too is not possible on a normal QQQ instrument but a rather a trap based equipment. Hence to allow broader participation please remove this specification since it is a lockout spec.	MS/MS/MS Scan is a very powerful tool to obtain structural information of many compounds of interest as secondary fragment ion is useful to distinguish the structures of the target analytes. Some applications include a) De novo sequencing of peptide b) O-Glycopeptide quantification in plasma c) In-depth study of protein glycosylation MS3 is possible by in source fragmentation followed by CID in a dedicated collision cell No change
7	4.2.18	Compatibility with Ion mobility.	The system should be compatible with Ion mobility as part of the module which adds the additional dimension of separation, for separating the	Kindly remove this specification since this upgradation possibility is not available with any vendor but one.	removed

			isobaric compounds/ co-eluting compounds, improving the spectra quality, to detect molecules at low levels or resolve chimeric spectra.	It is locking the spec in favor of that vendor exclusively.	
8	4.2.19	Operating Modes	MS/MS/MS or MS3 for complex challenging molecule	Please note that this feature is unique to only one vendor and that too is not possible on a normal QQQ instrument but a rather a trap based equipment. Hence to allow broader participation please remove this specification since it is a lockout spec.	MS/MS/MS Scan is a very powerful tool to obtain structural information of many compounds of interest as secondary fragment ion is useful to distinguish the structures of the target analytes. Some applications include a) De novo sequencing of peptide b) O-Glycopeptide quantification in plasma c) In-depth study of protein glycosylation No change
			For untargeted screening workflow system should have the capability to quantify as well as simultaneously screen metabolites/compounds using MRM/SRM triggered product ion spectrum of potential metabolites in DDA/IDA mode at high scan rate of 20,000Da/sec or better with provision of generating higher resolution (~9000FWHM) spectrum.	PLease note untargeted workflow cannot be performed on a QQQ instruemnt. Kindly change the scan speed to 17000 or better since at 17000Da/sec we can already generate upto 25-30 datapoints on a 5sec UHPLC peak; whereas the requirement from most regulatories is only 10-12 points.	The instrument is not going to be used for only regulatory applications but planned for discovery mode untargeted operations as well No change

				hence application wise it wont be must different.	
9	HPLC - 7	Flow rate precision	0.06% RSD	Kindly change to 0.07%	Changed to 0.07%

All the concerns indicated by Sciex against the published specifications were discussed in the pre-Bid meeting in presence of representatives from Agilent and Sciex. Summarized below:

4.2.8	Source Ionization Technology	The LC-MS/MS System should have interchangeable ionization source (ESI & APCI) to cater broader range of applications and carrying out MS and MS/MS experiments. The source will have orthogonal spraying for improved robustness and avoid contamination for versatile application requirements. ESI & APCI source flow rate range compatibility in ESI mode should be from 5 µL/min to 3000 µL/min or better and APCI mode from 50 µL/min to 3000 µL/min or better, without flow splitting in both positive and negative mode.	Sciex requested to change 50ul/min to 3000 ul/min to 200 ul/min to 3000 ul/min	Changed to 200 ul/min to 3000 ul/min
	Computer and software Point B.3 Software features	Libraries for metabolites, lipids etc	Sciex requested change to 'Libraries/database for metabolites, lipids etc'	Changed to Libraries and database for metabolites, lipids etc

(MOHIT SHARMA) 13/12/2023

SHOBHIT 13.12.23 (SHOBHIT)

13/12/23 Arun Kumar

13/12/23 Shesh Kumar

Bidders attendance sheet for PBC scheduled on 13.12. 2023 at 11:00 AM onwards.

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Description of the work: Supply and installation of Triple Quadrupole Mass Spectrometer

Sl. No.	Name of the Firm	Name of the Representative	Signature
1	Agilent	Arun Kumar P	13.12.23
2	Agilent	Ghesh Kumar	13.12.23
3.	Sciex	Bhavya Shukla	13/12/2023
4	SCIEX	Shobhit	Shobhit 13.12.2023
5	Sciex	Dipankar Malakar	13.12.2023
6	Sciex	Mohit Sharma	13/12/23