[INSTRUMENT SPECIFICATIONS]

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SYNAPT G2-S*i* MS System

SYNAPT® G2-S*i* MS provides the most uncompromising High Resolution UPLC®/MS/MS performance, with the greatest versatility and upgrade option to access three dimensions of resolution for the ultimate in discovery power.

SYNAPT G2-S*i* combines revolutionary StepWave™ ion optics with proven Quantitative Tof (QuanTof™) and High Definition Mass Spectrometry® technologies to provide the highest levels of sensitivity, selectivity, and speed. With Waters leading MS Informatics, SYNAPT G2-S*i* will help you efficiently extract the maximum information from your most challenging samples with high performance untargeted (UPLC/MS^E) or targeted (DDA and Tof-MRM) workflows.

SYNAPT G2-S*i* MS is a high resolution exact mass MS/MS platform designed to get you to the right result, faster – no matter how challenging your application is – whether you specialize in metabolite profiling, proteomics, biomarker discovery, biopharmaceuticals, or screening applications.

SYNAPT G2-S*i* MS can also be upgraded on-site to incorporate full SYNAPT High Definition MS capability to provide the added benefit of high-efficiency T-Wave™ ion mobility separations to your discovery applications.

SYSTEM HARDWARE SPECIFICATIONS

Regulatory approvals/marks	CE, CB, NRTL (CAN/US), RCM

PERFORMANCE SPECIFICATIONS

The SYNAPT G2-S*i* MS System operates in TOF mode and can be upgraded on site to provide Mobility-TOF mode

TOF mass resolution in positive ion	60,000 FWHM measured on the $(M + 6H)^{6+}$ isotope cluster from bovine insulin (*m/z* 956)
TOF mass resolution in negative ion	60,000 FWHM measured on the $(M - 4H)^{4-}$ isotope cluster from bovine insulin (*m/z* 1431)
Positive ion MS sensitivity	The peak at *m/z* 556 from a solution of 50 pg/µL leucine enkephalin in 50/50 acetonitrile/water +0.1% formic acid, infused at a flow rate of 5 µL/min, will have an intensity of greater than 31,200 ions per second. The instrument will be tuned to 10,000 resolution (as demonstrated on bovine insulin) and the mass range will be set to a maximum of 1200 *m/z* **Target Enhancement mode** The peak at *m/z* 556 from a solution of 10 pg/µL leucine enkephalin in 50/50 acetonitrile/water +0.1% formic acid, infused at a flow rate of 5 µL/min, will have an intensity of greater than 24,800 ions per second. The instrument will be tuned to 20,000 resolution (as demonstrated on bovine insulin), with sensitivity set to a maximum at 556 *m/z*

Negative ion MS sensitivity	The peak at *m/z* 503 from a solution of 500 pg/µL raffinose in 70/30 acetonitrile/water (no additives), infused at a flow rate of 5 µL/min, will have an intensity of greater than 33,600 ions per second. The instrument will be tuned to 10,000 resolution (as demonstrated on bovine insulin), and the mass range will be set to a maximum of 1200 *m/z*
Positive ion MS/MS sensitivity	Using a [Glu^1] -Fibrinopeptide B solution of 100 fmol/µL, at a flow rate of 5 µL/min and with the instrument tuned for 10,000 resolution (as demonstrated on bovine insulin), the intensity of the most intense y" sequence ion from the MS/MS spectrum of the doubly charged precursor ion (785.8 *m/z*) will be greater than 2,400 ions per second. The instrument mass range will be set to a maximum of 2000 *m/z*
Negative ion MS/MS sensitivity	Using a solution of 500 pg/µL raffinose in 70/30 acetonitrile/water, at a flow rate of 5 µL/min and with the instrument tuned for 10,000 resolution (as demonstrated on bovine insulin), the intensity of the fragment ion at 179.1 *m/z* in the MS/MS spectrum of the precursor ion at 503.2 *m/z* will be greater than 2,400 ions per second. The instrument mass range will be set to a maximum of 1200 *m/z*
Mass scale calibration accuracy	The mass measurement accuracy of the instrument in High Resolution mode, using internal lock masses, is such that the RMS error between the measured and the accepted masses of peaks which have sufficient intensity, and are free from interference from other masses, will be less than 1 ppm over the range 150 to 900 *m/z*
Mass measurement accuracy	The mass measurement accuracy of the instrument, in High Resolution mode, will be better than 1 ppm RMS, based on 10 consecutive repeat measurements of the [M + Na]$^+$ ion of raffinose (*m/z* 527.1588), using the [M + H]$^+$ ions of leucine enkephalin (*m/z* 556.2771) and 4-acetamidophenol (*m/z* 152.0712) as the LockSpray™ lockmasses. Analyte and lockmass peaks must have sufficient intensity and be free of interference from other masses
Mass range	The TOF mass range is 20 to 100,000 *m/z* in Resolution mode, and 20 to 32,000 *m/z* in High Resolution mode. The *m/z* transmission range for a quadrupole in non-resolving mode is 20 to 16,000 *m/z* for a 4000 *m/z* quadrupole, and 20 to 32,000 *m/z* for an 8000 *m/z* quadrupole
Acquisition rate	Mass spectra can be acquired up to a rate of 30 per second (mode dependent)
Dynamic range	The dynamic range in High Resolution mode, defined as the range of peak intensities that will give better than 3 ppm accurate mass RMS for 10 sec of data without pDRE (programmable Dynamic Range Enhancement), is at least 4 orders of magnitude, when measured on the *m/z* 556.2771 peak from leucine enkephalin
High mass precursor selection	Applicable to instruments with 8000 *m/z* and 32,000 *m/z* quadrupoles only The low energy MS/MS spectrum of *m/z* 5569.1 from a solution of 2 µg/µL sodium iodide in 50/50 isopropanol/water will contain only *m/z* 5569.1 and its fragments. The intensity of the largest fragment ion will be less than 5% of the intensity of the precursor ion. MS/MS data will be acquired over the mass range 100 – 8000 *m/z*, with collision energy of 10 eV

MALDI PERFORMANCE SPECIFICATIONS

Mass resolution in positive ion	35,000 measured on the [M + H]+ isotope cluster from insulin B chain (*m/z* 3494.6)
Mass resolution in negative ion	35,000 measured on the [M - H]- isotope cluster from insulin B chain (*m/z* 3492.6)
Positive ion MS sensitivity	The peak at *m/z* 1570.6774 from 10 fmol of [Glu^1] -Fibrinopeptide B will have an intensity of greater than 24,000 counts acquired from an entire line through a sample well. The instrument *m/z* range will be set to 2000 When this combined acquisition is smoothed (5 window, 1 number Savitzy Golay) and backgroundsubtracted the signal-to-noise ratio will be greater than 90:1 when compared to a region of the *m/z* scale between 1768 and 1818
Negative ion MS sensitivity	The peak at *m/z* 1568.6618 from 100 fmol of [Glu^1]-Fibrinopeptide B will have an intensity of greater than 24,000 counts acquired from an entire line through a sample well. The instrument *m/z* range will be set to 2000 When this combined acquisition is smoothed (5 window, 1 number Savitzy Golay) and background subtracted the signal-to-noise ratio will be greater than 90:1 when compared to a region of the *m/z* scale between 1768 and 1818
Positive ion MS sensitivity	Measured in Sensitivity mode The peak at *m/z* 1056.4750 (y9) from 10 fmol of [Glu^1] -Fibrinopeptide B will have an intensity of greater than 750 counts for an entire line through a sample well. The instrument *m/z* range will be set to 2000 (Precursor+50) and the collision energy and instrument conditions set such that the intensity of this peak will be greater than 40% of the intensity of the precursor peak When this combined acquisition is smoothed (5 window, 1 number Savitzy Golay) and background subtracted the signal-to-noise ratio should be greater than 60:1 for the *m/z* 1056.4750 peak when compared to a region of the *m/z* scale between 1450 and 1490
Mass measurement	Measured in Sensitivity mode, positive ion The mass measurement accuracy will be better than 1 ppm RMS, measured from a mixture of PEG oligomers between *m/z* 700–2500; using an internal reference peak and an instrument calibration that covers the same mass range

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