

## Center Instrumentation (Overview)

### Instrumentation

Instrument	Yr	Ionization Source(s) & Mass Analyzer Type(s)	General Applications	Pictures
Waters Micromass Synapt HDMS MassLynx 4.1 Windows <sup>XP</sup> OS	2008	± ESI (QT™ oa-TOF) MS/MS Tandem Hybrid MS	Cap-LC combined with ion mobility separations (IMS) & Q-ToF MS, enabling the differentiation of analytes by size, shape, charge, and mass.	[28].jpg
Waters Micromass Quattro Micro API MassLynx 4.1 - Windows <sup>XP</sup> OS	2008	± ESI & APCI (QH) MS/MS Tandem Quadrupole MS	Automated LC/MS/MS quantification. Drug metabolism studies. Analysis of complex biological extracts.	[32].jpg
Micromass Quattro Premier XE MassLynx 4.1 - Windows <sup>XP</sup> OS	2006	± ESI & APCI (QT)MS/MS Tandem Quadrupole MS	Automated LC/MS/MS quantification. Drug metabolism studies. Analysis of complex biological extracts.	[33].jpg
Shimadzu QP2010 / GCMS Solutions 2.21 - Windows <sup>XP</sup> OS	2006	± EI & CI (Q)MS Quadrupole MS	Automated GC/MS quantitative and qualitative analysis. Drugs, metabolites, synthetic and natural products.	[34].jpg
Thermo LTQ-OT / * Xcalibur 2.0 – Windows <sup>XP</sup> OS	2006	± ESI LTQ Orbitrap MS/MS Fourier transform Tandem Hybrid MS	Capillary LC/MS/MS of proteolytic digests of simple and complex mixtures	[50].jpg
Thermo LTQ-FT / * Xcalibur 2.0 – Windows <sup>XP</sup> OS	2004	± ESI LTQ [FT(ICR)] MS/MS Fourier transform Tandem Hybrid MS	Capillary LC/MS/MS of proteolytic digests of simple and complex mixtures	[49].jpg
Bruker AutoFlex II / Compass 1.0 - Windows <sup>XP</sup> OS [31]	2004	± MALDI TOF MS Time of Flight MS	Characterization and identification of proteins by peptide mass mapping. PSD peptide sequencing.	[31].jpg

<b>Micromass Platform LCZ / MassLynx 3.4 – Windows NT OS [30]</b>	<b>2004</b>	<b>± ESI &amp; APCI (Q)MS Quadrupole MS</b>	Fully automated quantitative analysis of drugs and metabolites.	<b>[30].jpg</b>
<b>Bruker APEX Qe 47 / Xmass 7.0.8 - Windows 2000 OS [27]</b>	<b>2002</b>	<b>± ESI QH [FT(ICR)] MS/MS Fourier transform Tandem Hybrid MS</b>	Identification & quantification of sample limited biologic materials by combined high resolution mass accuracy & high sensitivity	<b>[27].jpg</b>
<b>Agilent Technologies LC/MSD/ChemStation Windows<sup>XP</sup> OS [29]</b>	<b>1999</b>	<b>± ESI &amp; APCI (Q)MS Quadrupole MS</b>	Fully automated quantitative analysis of drugs and metabolites.	<b>[29].jpg</b>

\* Goodlett Laboratory Proteomic Core instrumentation operated within the Center.