

**German Financial Cooperation with the „Western Balkan Six Chamber Investment Forum” (WB6-CIF)
Regional Challenge Fund Project**

Supply Tender „Procurement of High-Performance Liquid Chromatograph (HPLC) coupled with Triple Quadrupole Mass Spectrometer (MS-MS) with Electrospray ionization (ESI) and Atmospheric pressure chemical ionization (APCI) source and Nitrogen generator “

Europe (non-EU), Serbia (SER)
Reference number: 509186

The answers to requests for clarifications received by the potential bidders to the following e-mail address: procurement@rcf-wb6.org

Q1	<p>1. Specification: Mass range: minimum m/z 5-3000 Exchange: Mass range: minimum m/z 2- 2000</p> <p>Clarification:</p> <p>In customers answer to exchange mass range, customer claims following: „since minimum 2 suppliers can meet the required specification, also for some planned peptides and protein fragments analysis, the beneficiary institution needs m/z mass range above 2000.“</p> <p>Reviewing professional literature, scientific articles and also application notes from different manufacturers of LCMSMS (which is subject of supply), it is visible and proven that for peptides and protein analysis upper range of mass range is around 1000. Please find attached application notes from Agilent, Thermo and Shimadzu where it is clearly stated that mass range used for the analysis for the peptides and protein fragments analysis is up to 1200 m/z using LCMSMS technique. (Attachment – LCMSMS application notes – peptides and protein fragments). As client can see, there is no need for higher mass range than proposed in the specification exchange.</p> <p>Furthermore, for peptide and protein analysis for higher mass range (above 2000 m/z), recommended technique for determinations is LCMS-QTOF/Orbitrap. Please find attached also application notes from Agilent, Thermo and Shimadzu for QTOF analysis of peptides with mass range above 2000 m/z. (Attachment – QTOF (Orbitrap) application notes – peptides and protein fragments).</p> <p>Since the subject of supply is LCMSMSM, proposed specification exchange (mass range 5-2000 or above) does not reduce the quality of the LCMSMS in no way, it enables the purchase of the high-end model of the instrument but under the most economically acceptable conditions which is in the interest of the client.</p>
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<p>A1</p>	<p>Section VII. Schedule of Requirements, point 3. Technical Specifications of the published supply tender will not be modified.</p> <p>The customer stays at its request for mass range (m/z 5-3000). We do not agree with your clarification. A review of literature shows that for many classes of polymers (peptides, polyols, nucleic acids, protein complexes etc.) triple quadrupole instruments have been and are used to analyse ions over m/z 2000. Due to inherent low noise in this part of the spectrum (which makes it quite practical for analysis) and the current trend of reducing charge envelopes with proton transfer reagents (which simplifies the spectra, but shifts the m/z to higher values for multiply charged species) the flexibility that is brought by a higher mass range cannot be overlooked and therefore specification from m/z range 5-3000 remains the same as requested. Lowering the mass range would limit the analytical possibilities of the facility.</p> <p>References:</p> <p>König, S., & Fales, H. M. (1998). Formation and decomposition of water clusters as observed in a triple quadrupole mass spectrometer. <i>J Am Soc Mass Spectrom</i> 1998, 9, 8, 814–822. doi:10.1016/s1044-0305(98)00044-0</p> <p>Collings, B. A., & Douglas, D. J. (1997). An extended mass range quadrupole for electrospray mass spectrometry, <i>International Journal of Mass Spectrometry and Ion Processes</i>, Volume 162, Issues 1–3, 1997, Pages 121-127, doi:10.1016/s0168-1176(96)04478-3</p> <p>Ji, Q. C., Rodila, R., Gage, E. M., & El-Shourbagy, T. A. (2003). A Strategy of Plasma Protein Quantitation by Selective Reaction Monitoring of an Intact Protein. <i>Analytical Chemistry</i>, 75(24), 7008–7014. doi:10.1021/ac034930n</p> <p>Cargile, B. J., McLuckey, S. A., & Stephenson, J. L. (2001). Identification of Bacteriophage MS2 Coat Protein from <i>E. coli</i> Lysates via Ion Trap Collisional Activation of Intact Protein Ions. <i>Analytical Chemistry</i>, 73(6), 1277–1285. doi:10.1021/ac0007251</p> <p>Wohlgemuth, I., Lenz, C., & Urlaub, H. (2015). Studying macromolecular complex stoichiometries by peptide-based mass spectrometry. <i>PROTEOMICS</i>, 15(5-6), 862–879. doi:10.1002/pmic.201400466</p>
<p>Q2</p>	<p>Is it possible to offer a system whose sensitivity is measured without a column, given that it has no effect on sensitivity in factory testing. If you remain with the request, please specify the exact chromatographic and ionization conditions so that the requested documentation can also be offered by other manufacturers of equipment whose testing differs from the one written.</p>
<p>A2</p>	<p>In line with Section VII. Schedule of Requirements, point 3. Technical Specifications: “Yes, it is possible to offer a system whose sensitivity is measured without a column, given that it has no effect on sensitivity in factory testing.”</p>