Mass spectrometry instrumentation timsTOF Pro 2 system (Bruker)

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Descriere: It is possible to publish a procurement notice in the Hilma and TED web pages of a direct purchase which is valued 215.000€ (VAT 0%) or more. If nobody challenges the direct purchase decision in 14 days then the direct purchase will have legal protection over possible future challenges. Also a contract award notice should be made of the direct purchase. A procurement notice has been published of the direct purchase in the Hilma – portal.Justification for the direct purchase. The justification must be based on one of the preconditions mentioned in the procurement act (1397/2016).(40§, 41§, 110§, 119§). 40§ 2) only a certain supplier can implement the procurement for a technical reason, or for a reason related to protecting an exclusive right; it shall be a further condition that there are no reasonable alternatives or substitute solutions, and that the absence of competition is not due to an artificial narrowing of the terms and conditions of the procurement.Mass spectrometry (MS) is a powerful analytical technique used to quantify known materials, to identify unknown compounds, and to elucidate the structure or chemical properties of different molecules. We have Thermo´s Orbitrap-mass spectrometer and Sciex´s TripleTOF 6600 -instrument that are widely used in the proteomic service and research projects. However, the coverage of complete proteomes is still very challenging due to the limited speed, sensitivity and resolution of current mass spectrometers. We recently acquired a previous version of the timsTOF Pro -line mass spectrometer and the improvements were massive, allowing us for first time almost complete characterization of organismal proteomes. The next instrument to be purchased must be of the QTOF type with ion mobility separation. Ion mobility is a great extension to MS that delivers information about the three-dimensional structure of an ion and increases peak capacity and confidence in compound characterization. Other needed features are;1) The instrument can synchronize the quadrupole with the IMS elution time to allow for a high MS/MS acquisition speed, leading to an increased fragmentation depth and there must be algorithms for intelligent targeting of low-level precursors2) The MS instrument must be capable of real-time data acquisition a data processing, enabling a high spectrum repetition rate of >100Hz in MS/MS mode (including ion 2 (2) mobility separation and without sacrificing sensitivity) to obtain highest possible identification of both peptides and proteins, i.e. achieving high sequence coverage of the identified proteins3) Mass resolution 60000 independent of MS or MS/MS sequencing speed4) Reproducibility of Collisional Cross Section (CCS) value determination <0.5 % RSD5) Pre-defined methods for DDA, DIA, PRM delivered, where both m/z and ion mobility are used for selectivity (i.e. window selection in DIA and PRM, and possibility to integrate various LC vendors into the instrument control software and the data-file format must be open architecture to enable easy input for various bioinformatics approaches in-house.The timsTOF Pro system comes with a dual-TIMS (trapped ion mobility spectrometry) analyzer optimized for high-speed shotgun proteomics. Its unique geometry allows incoming ions to be accumulated in parallel in the first section, and for ions to be released dependent on their mobility from the second section of the dual-TIMS analyzer. This results in nearly 100% duty cycle, making this parallel accumulation serial fragmentation technique (PASEF) perfectly suited for nanoflow LC-MS analysis of enzymatically digested complex protein mixtures. The timsTOF Pro system provides unique technology for identification of peptides which is highly relevant for our research.The timsTOF Pro 2 from Bruker is the only system in the market that has TIMS technology allowing PASEF, dia-PASEF and prm-PASEF acquisition methods, and has the abovementioned essential features. We also have applications where we plan to use this instrument in conjunction with Evosep One HPLC system in a clinical research that measures proteins from various patient samples faster and more robustly. Globally the MS analyses are concentrating on running bigger sample cohorts, and thus increased sample acquisition capacity with method transferability is an absolute key and justifies this purchase.