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## **Recommended criteria for the mass spectrometric identification of target peptides and proteins (< 8 kDa) in sports drug testing**

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### **Extended Abstract**

Mass spectrometry has become an invaluable tool for the identification of prohibited peptide hormones and proteins in doping control analysis. Regulatory authorities have established criteria for identifying banned drugs in doping control specimens, but these criteria do not address specifics for high molecular weight protein drugs such as molecular weight determination of multiply charged molecules, analysis of chemically or enzymatically derived degradation products, identification of amino acid sequence tags, etc. Technical considerations such as sample preparation methods (e.g. immunoaffinity purification), resulting analytes (e.g. intact compounds vs. chemically or enzymatically derived peptides), ionization modes, analyzer resolution, and the information provided by respective techniques necessitate discussion in light of sports drug testing requirements. An alternative approach based on so called identification points (IPs) is suggested as adapted from earlier proposals considering low molecular weight drugs also. In contrast to currently applied WADA criteria, IPs consider the differences in identification power of low resolution, high resolution/high accuracy, MS and MS<sup>n</sup> techniques. A minimum of three (3) IPs was suggested for small analyte identification, which can be accomplished also as a sum of different derivatives and

analyses. However, considering the complexity of peptide and protein identification, a minimum of 5 IPs is recommended for sports drug testing applications, if these parameters, which are currently not applied in doping controls, shall be used to target analyte characterization in the future. Nevertheless, general requirements for each ion or product ion as required by WADA guidelines such as S/N ratio or relative abundance must be fulfilled too.

*For further details please refer to*

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