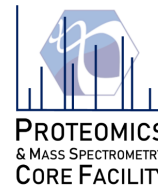


Intact protein/peptide mass determination by ESI-MS Submission Form

Proteomics and Mass Spectrometry Core Facility
Malopolska Centre of Biotechnology, Jagiellonian University
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User Information					
Name:			Date:		
Mail:			Phone:		
Institution:			Group name (PI):		
Sample Details					
Purpose of experiment:					
No	Eppendorf mark	Approximate Molecular weight [Da]	Buffer composition	Concentration and volume	Additional information (e.g. sequence, purification history, mutations, modifications)
1		<input type="checkbox"/> Average: <input type="checkbox"/> Monoisotopic:			
2		<input type="checkbox"/> Average: <input type="checkbox"/> Monoisotopic:			
3		<input type="checkbox"/> Average: <input type="checkbox"/> Monoisotopic:			
4		<input type="checkbox"/> Average: <input type="checkbox"/> Monoisotopic:			
5		<input type="checkbox"/> Average: <input type="checkbox"/> Monoisotopic:			
...					

Please remember:

- Users are responsible to fulfill all legal, ethical and regulatory standards associated with the samples and ensure proper anonymization of sample identifiers. By providing samples to the Core Facility, you confirm that all relevant consents, licenses or approvals have been obtained (including GMM/GMO approval and/or Bioethics Committee approval).
- Collaborative projects that require non-routine sample preparation or in-depth data analysis justifies a coauthorship on a manuscript that contains data generated in the facility. Staff members involved in such projects are expected to be included as co-authors in the publication process.
- Apart from collaborative projects, all users are required to acknowledge the Core Facility if any data obtained in the facility has been used in posters, articles, or other publications. For example, please use the following wording:
We acknowledge Proteomics and Mass Spectrometry Core Facility of the Malopolska Centre of Biotechnology, Jagiellonian University for mass spectrometry analysis.