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Title:	Direct N-terminal sequencing of polypeptides using a thermostable bacterial aminopeptidase and MALDI-TOF mass spectrometry
Authors:	Kishor, Nitin (/jspui/browse?type=author&value=Kishor%2C+Nitin) Guptasarma, P. (/jspui/browse?type=author&value=Guptasarma%2C+P.)
Keywords:	Bacillus subtilis aminopeptidase MALDI-TOF mass spectrometry Non-specific aminopeptidase Peptide N-terminal sequencing
Issue Date:	2015
Publisher:	Science Direct
Abstract:	Mass spectrometry-based amino acid sequencing is currently based almost entirely on collision-induced peptide fragmentation and analyses. Here, we describe a single-stage MS-based technique for amino acid sequencing involving partial, heterogenous digestion of a peptide by a processive, non-specific, heat-loving Bacillus subtilis-derived aminopeptidase (BsuAP), which acts optimally at 70 °C and allows 'single-shot' sequencing to be carried out through simultaneous accumulation, and detection of sub-populations of peptides of progressively reducing length
URI:	<a href="https://www.sciencedirect.com/science/article/pii/S0003269715003449">https://www.sciencedirect.com/science/article/pii/S0003269715003449</a> ( <a href="https://www.sciencedirect.com/science/article/pii/S0003269715003449">https://www.sciencedirect.com/science/article/pii/S0003269715003449</a> ) <a href="http://hdl.handle.net/123456789/2799">http://hdl.handle.net/123456789/2799</a> ( <a href="http://hdl.handle.net/123456789/2799">http://hdl.handle.net/123456789/2799</a> )
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