

Abstract Submitted
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Sequencing proteins with transverse ionic transport PAUL BOYNTON, MASSIMILIANO DI VENTRA, University of California, San Diego — *De novo* protein sequencing is essential for understanding cellular processes that govern the function of living organisms. By obtaining the order of the amino acids that composes a given protein one can determine both its secondary and tertiary structures through protein structure prediction, which is used to create models for protein aggregation diseases such as Alzheimer's Disease [1]. Mass spectrometry is the current technique of choice for *de novo* sequencing, but because some amino acids have the same mass the sequence cannot be completely determined in many cases. In this paper we propose a new technique for *de novo* protein sequencing that involves translocating a polypeptide through a synthetic nanochannel and measuring the ionic current of each amino acid through an intersecting perpendicular nanochannel, similar to that proposed in [2] for DNA sequencing. Indeed, we find that the distribution of ionic currents for each of the 20 proteinogenic amino acids encoded by eukaryotic genes is statistically distinct, showing this technique's potential for *de novo* protein sequencing.

[1] Kelley, Nicholas W., et al. The Journal of Chemical Physics 129 (2008): 214707.

[2] Wilson, James, and M. Di Ventra. Nanotechnology 24 (2013): 415101.

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