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On the cover, the automated analysis of unsequenced proteins remains hindered by restrictive or error-prone sequencing techniques. We show that, not unlike the way the assembly of DNA reads into genomics sequences, unidentified MS/MS spectra can be assembled into protein contigs to greatly increase the length and quality of the reconstructed protein sequences, as demonstrated on a sample of western diamondback rattlesnake venom extract. For details, see article by Bandeira *et al.*, pages 1123–1134.

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