Samples are analyzed using a ThermoScientific Q Exactive Plus Orbitrap mass spectrometer with inbuilt Proxeon nanospray and Proxeon Easy-nLC II HPLC. The digested samples (750 ng) are loaded on a 100 μm × 25 mm Magic C18 100 Å 5 U reverse phase trap, desalted online and separated over 140-min gradient via 75 μm × 150 mm Magic C18 200 Å 3 U reverse phase column at 300 nL/min flow rate. The solvent gradient for the elution of peptides begins with 5% ACN and increases linearly to 20% ACN at 92 minutes, 32% ACN at 112 minutes, and 80% ACN at 119 minutes. The 80% ACN solvent ratio is then held for 10 minutes, and then taken back down to 5% at 130 minutes and held for 10 minutes. MS survey is conducted at the m/z range of 350-1600, and the 15 most abundant ions from the spectra are selected and subjected to higher-energy C-trap dissociation (HCD) to fragment the precursor peptides and obtain MS/MS spectra. Precursor ions selected in a 1.6 m/z isolation mass window are fragmented via 27% normalized collision energy. A15 s duration was used for dynamic exclusion.

This information was retrieved from the following manuscript:

Borja, T., Karim, N., Goecker, Z., Salemi, M., Phinney, B., Naeem, M., Rice, R., Parker, G. (2019). Proteomic Genotyping of Fingermark Donors with Genetically Variant Peptides. Forensic Science International: Genetics https://doi.org/10.1016/j.fsigen.2019.05.005