

Protein score, from a single plasma sample, predicts atherosclerotic cardiovascular disease

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In a large retrospective analysis using measurements of thousands of plasma proteins in primary and secondary event populations, scientists

from deCODE genetics and collaborators from U.S., Denmark and Iceland, reported today in *JAMA* how they employed AI to develop a protein score to predict major atherosclerotic cardiovascular disease events (ASCVD).

The study is based on a large data set consisting of over 13,500 Icelanders who had not experienced major ASCVD before plasma sampling and over 6,000 participants in the FOURIER trial who had suffered ASCVD before plasma sampling. All of these samples had measurements of the levels of around 5,000 [plasma proteins](#) measured with the SomaScan platform.

The protein risk score, which is solely based on proteomics data from a single plasma sample, predicts ASCVD events well in the absence of information on [medical history](#) and [risk factors](#). A large part of the risk captured by the proteins is also captured by established risk factors, however, the protein score captures additional risk.

What is more, the protein risk score is a dynamic measure and as such has the potential of being modified upon treatment unlike some of the classic risk factors that are immutable, such as family history and prior ASCVD events. This dynamic feature of protein risk scores, that the levels of proteins rise and fall as a function of time to and from events, makes it well-suited to predict the timing of events.

As a result, protein risk scores could become an important tool in [clinical trials](#) to get an early assessment of the efficacy of therapeutic intervention or for monitoring risk.

"We believe that in the proteomic risk score, we may have a biomarker that will allow the world to conduct shorter clinical trials with fewer participants. This is going to make the development of new medicines less expensive and make them available sooner for those who need them.

Furthermore, in [clinical practice](#) it may allow for more effective prevention of ASCVD," said Kari Stefansson, CEO of deCODE genetics and one of the senior investigators of the study.

More information: Hannes Helgason et al, Evaluation of Large-Scale Proteomics for Prediction of Cardiovascular Events, *JAMA* (2023).
[DOI: 10.1001/jama.2023.13258](https://doi.org/10.1001/jama.2023.13258)

Provided by deCODE genetics

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