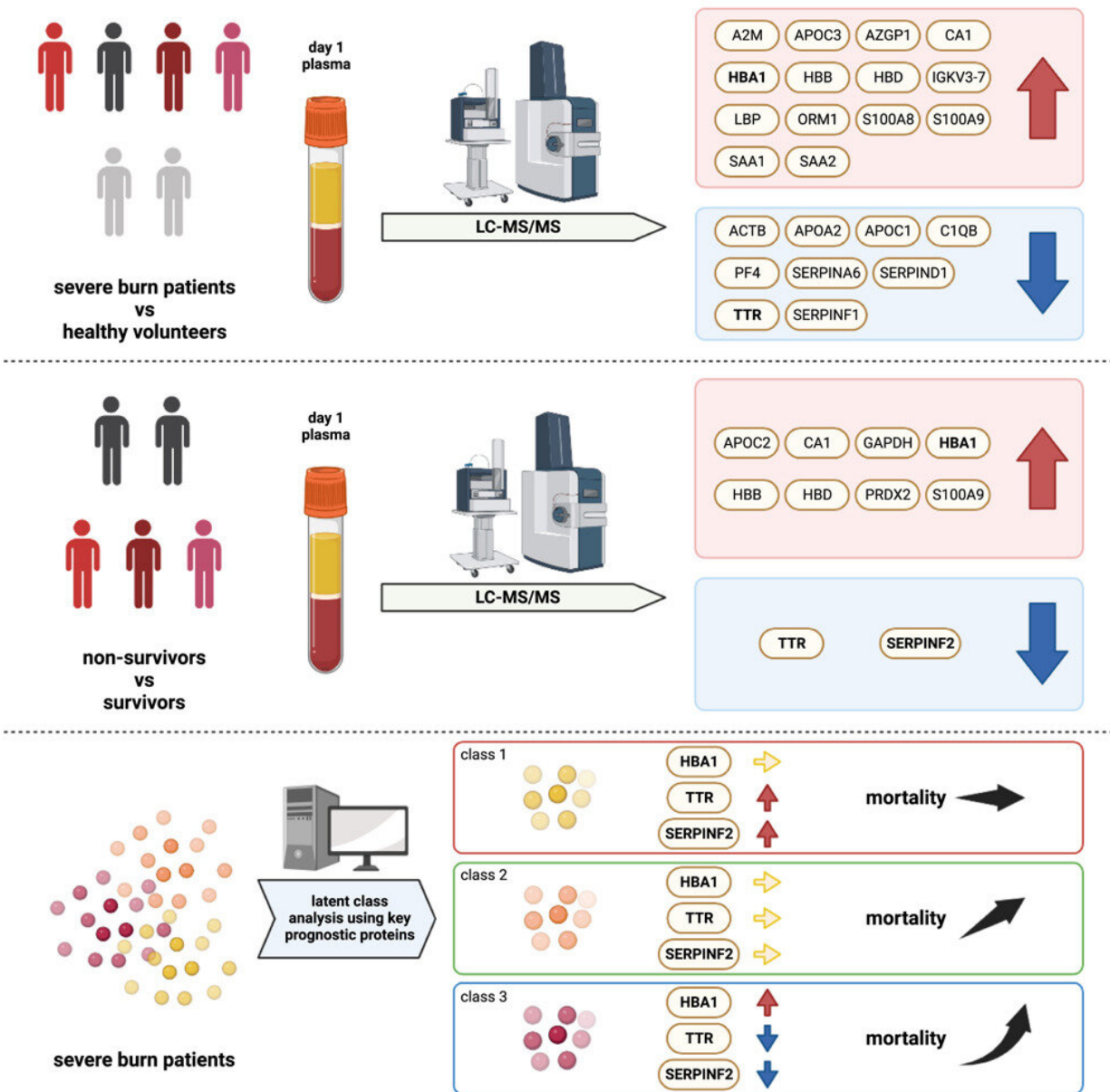


# Researchers identify proteins associated with deadly burns

July 18 2023



Graphical abstract. Credit: *iScience* (2023). DOI: 10.1016/j.isci.2023.107271

Although many people still die from severe burns, the underlying physiology behind burns is not well understood. In an article published in *iScience*, researchers from Osaka University identified key proteins associated with mortality in people with life-threatening burns.

Proteomics is the large-scale study of an organism's entire set of proteins. Recent developments in mass spectrometry—an analytic technique used to identify chemical substances—have improved the feasibility of proteomic analysis, enabling the identification of hundreds to thousands of proteins at a time.

Shinya Onishi, the study's lead author, emphasizes that proteomic analysis of burns is still in its infancy. "Burns are known to cause severe circulatory, immune, metabolic, and coagulation system dysregulation," he says. "For example, right after an injury, there is an immediate increase in capillary permeability, which is one of the main factors leading to circulatory failure. However, the details behind many of these mechanisms are still unclear."

The retrospective observational study included 10 healthy volunteers and 83 [burn](#) patients, 15 of whom died within 28 days of injury. Proteins in plasma samples were analyzed using [mass spectrometry](#). The authors then performed various statistical analyses to understand how differences in [protein levels](#) correlated with burn severity.

Jun Oda, a senior author of the study, highlights the two underlying goals of the study. "The first goal is to identify previously unidentified proteins that might be associated with the pathogenesis of life-threatening burns," he says. "The second goal is to investigate novel

molecular pathways in burn victims that might be the targets of future drugs."

Ultimately, 10 proteins were identified that were strongly associated with [mortality](#).

Furthermore, three of those proteins (HBA1, TTR, and SERPINF2) showed the highest association with mortality and were used by the researchers to classify patients (also known as clinical phenotyping) into three groups corresponding to [mortality rates](#). The group which had the highest mortality, was characterized by higher levels of HBA1 and lower levels of TTR and SERPINF2.

One of the proteins, HBA1, is associated with hemoglobin, while another, TTR, is an indicator of the breakdown of proteins in the body.

Finally, the third [protein](#), SERPINF2, is associated with the development and dissolution of blood clots. Onishi emphasizes that "these three proteins can function as important prognostic biomarkers for burn patients." Therefore, future research on these proteins and their pathways is necessary as they are promising targets for developing new therapeutic strategies and drugs for [severe burns](#).

**More information:** Shinya Onishi et al, Combination of HBA1, TTR, and SERPINF2 in plasma defines phenotype correlated with severe burn outcome, *iScience* (2023). [DOI: 10.1016/j.isci.2023.107271](https://doi.org/10.1016/j.isci.2023.107271)

Provided by Osaka University

Citation: Researchers identify proteins associated with deadly burns (2023, July 18) retrieved 27 April 2024 from <https://medicalxpress.com/news/2023-07-proteins-deadly.html>

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