compassionate use. Hemoglobin substitutes are cross-linked, polymerized, or conjugated human or bovine hemoglobin (1), and they impart a reddish brown color. Jehovah’s Witnesses will not accept blood fractions (red blood cells, plasma, platelets, granulocytes). Acceptable treatments include crystalloids, vasopressors, and hemostatic products (2). Unlike the point-of-care measurement, the core laboratory included a correction for hemolysis. Because this correction subtracted free hemoglobin (or blood substitute), we considered the point-of-care result correct.

Author Contributions: All authors confirmed they have contributed to the intellectual content of this paper and have met the following 3 requirements: (a) significant contributions to the conception and design, acquisition of data, or analysis and interpretation of data; (b) drafting or revising the article for intellectual content; and (c) final approval of the published article.

References

News & Views

A Standardized Open-Source Mass Spectrometry Toolkit: Potential for Facilitating Proteomics Research

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In October 2012, Nature Biotechnology published an article by Chambers and colleagues describing the ProteoWizard Toolkit (1). Despite the successes of mass spectrometry–based proteomics, the interpretation of massive data sets remains a challenge. The open-source Toolkit provides a set of software libraries and interfaced applications robust enough to potentially bridge all of the common data formats of mass spectrometry vendors, a recognized hindrance to the development of proteomic software tools for facilitating proteomics data analysis. Although the development of previously described “open” formats has suffered from several limitations, Chambers and colleagues mitigate these challenges through open-source, permissively licensed, cross-platform software that is robust enough to be used in both academic and commercial projects. This repository, where proteomics software developers can share their work, uses a modular framework of many independent libraries grouped in dependency levels. The Data, Utility, and Analysis layers within the modular structure of the Toolkit are responsible for interfacing with mass spectrometry data, performing computations, and providing common proteomics-centric analysis modules, respectively. In addition to describing handling computations for chemical formulas, peptide calculations, and isotope envelopes, this article also highlights examples of the Toolkit in action. ProteoWizard boasts data library access and browsing and printing capabilities through a common language infrastructure for peptide- and protein-identification data, performance of in silico digests of a protein read, and data-access capabilities that can enable mass spectrometry–based problem solving beyond proteomics investigations. Additional available analysis classes are described. Work is ongoing to collaboratively create a modular-analysis infrastructure in which experts will be able to
contribute a module that can then be plugged into various software tools. The ProteoWizard Toolkit design provides analytical tools that facilitate the promise of a standardized mechanism for sharing proteomic mass spectrometry data in the research community.

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