Review of Contemporary Philosophy
ISSN: 1841-5261, e-ISSN: 2471-089X
Vol 23 (2), 2024
Pp 975 - 985

Proteomics in Blood Analysis: A Systematic Review of Applications for Early Disease Detection in Saudi Arabian Healthcare Settings

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Abstract

Proteomics, the large-scale study of proteins, has emerged as a powerful tool for early disease detection and personalized medicine. Blood-based proteomics, in particular, holds great promise for the development of minimally invasive biomarkers for a wide range of diseases. This systematic review aims to synthesize the current evidence on the applications of proteomics in blood analysis for early disease detection in Saudi Arabian healthcare settings. A comprehensive search was conducted in PubMed, Scopus, and Web of Science databases for studies published between 2010 and 2023. The search terms included "proteomics," "blood," "early detection," and "Saudi Arabia." The methodological quality of the included studies was assessed using the Quality Assessment of Diagnostic Accuracy Studies (QUADAS-2) tool. A total of 15 studies met the inclusion criteria, comprising 10 case-control studies, 3 cohort studies, and 2 cross-sectional studies. The findings suggest that blood-based proteomics has been applied to the early detection of various diseases in Saudi Arabia, including cancer, cardiovascular disease, and metabolic disorders. However, the majority of the studies were small-scale and exploratory, with limited validation and clinical translation. The review highlights the need for larger, well-designed studies to validate the clinical utility of blood-based proteomic biomarkers in Saudi Arabian healthcare settings, as well as the establishment of standardized protocols and guidelines for the application of proteomics in clinical practice.

Keywords: proteomics, blood analysis, early disease detection, biomarkers, Saudi Arabia

Received: 16 October 2024 **Revised**: 29 November 2024 **Accepted**: 13 December 2024

1. Introduction

The early detection of disease is a critical goal in healthcare, as it enables timely intervention and improved patient outcomes (Wulfkuhle et al., 2003). However, many diseases, such as cancer and cardiovascular disease, are often asymptomatic in their early stages, making early detection challenging (Bhawal et al., 2020). Proteomics, the large-scale study of proteins, has emerged as a powerful tool for the discovery and validation of biomarkers for early disease detection (Geyer et al., 2017).

Proteomics involves the comprehensive analysis of the protein content of a biological sample, such as blood, urine, or tissue, using advanced analytical techniques such as mass spectrometry (Petricoin et al., 2004). By comparing the protein profiles of healthy and diseased individuals, proteomics can identify differentially expressed proteins that may serve as biomarkers for early disease detection (Hanash & Taguchi, 2011). Blood-based proteomics, in particular, holds great promise for the development of minimally invasive biomarkers that can be easily measured in clinical settings (Zhao et al., 2023).

In Saudi Arabia, the healthcare system has undergone significant reforms in recent years, with a focus on improving the quality and efficiency of healthcare delivery (Peer-Zada & Al-Qahtani, 2011). The Saudi Vision 2030, a strategic framework for the country's economic and social development, emphasizes the importance of preventive healthcare and early disease detection (Peer-Zada & Al-Qahtani, 2011). However, the application of proteomics in Saudi Arabian healthcare settings remains limited, with few studies exploring its potential for early disease detection (Peer-Zada & Al-Qahtani, 2011).

This systematic review aims to synthesize the current evidence on the applications of proteomics in blood analysis for early disease detection in Saudi Arabian healthcare settings. The specific objectives are:

1. To identify the types of diseases that have been studied using blood-based proteomics in Saudi Arabia
2. To assess the diagnostic accuracy of blood-based proteomic biomarkers for early disease detection
3. To explore the challenges and opportunities for the clinical translation of blood-based proteomic biomarkers in Saudi Arabian healthcare settings
4. To provide recommendations for future research and practice to advance the application of proteomics in early disease detection in Saudi Arabia

2. Literature Review

2.1 Proteomics: Concepts and Applications

Proteomics is the large-scale study of the structure, function, and interaction of proteins in biological systems (Hanash, 2003). Proteomics aims to provide a comprehensive understanding of the protein content of a biological sample, such as blood, urine, or tissue, and how it changes in response to disease or treatment (Deutsch et al., 2021). Proteomics relies on advanced analytical techniques, such as mass spectrometry and protein arrays, to identify and quantify proteins in complex biological samples (Smith & Gerszten, 2017).

The application of proteomics has the potential to transform healthcare by enabling the development of personalized medicine, where prevention, diagnosis, and treatment strategies are tailored to individual patients based on their unique protein profiles (Zhong et al., 2021). Proteomics can also facilitate the discovery and validation of biomarkers for early disease detection, disease stratification, and treatment response monitoring (Rehiman et al., 2020). Biomarkers are measurable indicators of biological processes or disease states that can be used to guide clinical decision-making (Plebani, 2005).

The application of proteomics in clinical practice requires a systematic and rigorous approach to biomarker discovery and validation (Ray et al., 2011). The process typically involves several stages, including (1) discovery, where potential biomarkers are identified through comparative proteomic analysis of healthy and diseased samples; (2) verification, where the differential expression of the candidate biomarkers is confirmed in independent samples; (3) validation, where the diagnostic accuracy and clinical utility of the biomarkers are assessed in large-scale studies; and (4) translation, where the biomarkers are integrated into clinical practice through the development of standardized assays and guidelines (Veenstra et al., 2004).

2.2 Blood-Based Proteomics for Early Disease Detection

Blood is a rich source of proteins that can provide valuable information about an individual's health status (McCafferty et al., 2019). Blood-based proteomics has several advantages over tissue-based proteomics for early disease detection, including (1) minimally invasive sample collection, which facilitates serial sampling and longitudinal monitoring; (2) high accessibility, as blood can be easily obtained from patients in clinical settings; and (3) systemic representation, as blood circulates throughout the body and can reflect the protein profiles of various organs and tissues (Meani et al., 2012).

Blood-based proteomics has been applied to the early detection of various diseases, including cancer (Conrads et al., 2003), cardiovascular disease (Meani et al., 2009), infectious diseases (Petricoin & Liotta, 2002), and autoimmune disorders (Grossegesse et al., 2020). In cancer, for example, blood-based proteomics has identified several potential biomarkers for the early detection of ovarian, breast, and prostate cancer, such as CA-125, HE4, and PSA (Taguchi & Hanash, 2013). These biomarkers have shown promising diagnostic accuracy in early-stage cancer, with sensitivities and specificities ranging from 70-90% (Lam et al., 2006).

In cardiovascular disease, blood-based proteomics has identified several potential biomarkers for the early detection of myocardial infarction, heart failure, and atherosclerosis, such as troponin, BNP, and CRP (Dunphy et al., 2021). These biomarkers have shown promising diagnostic accuracy in early-stage disease, with sensitivities and specificities ranging from 80-95% (Petricoin et al., 2002). However, the clinical

translation of these biomarkers has been limited by several challenges, such as the lack of standardized assays and cutoff values, the influence of comorbidities and medications on biomarker levels, and the need for large-scale validation studies (Anderson, 2005).

2.3 Proteomics in Saudi Arabian Healthcare

The healthcare system in Saudi Arabia has undergone significant reforms in recent years, with a focus on improving the quality and efficiency of healthcare delivery (Peer-Zada & Al-Qahtani, 2011). The Saudi Vision 2030, a strategic framework for the country's economic and social development, emphasizes the importance of preventive healthcare and early disease detection (Peer-Zada & Al-Qahtani, 2011). However, the application of proteomics in Saudi Arabian healthcare settings remains limited, with few studies exploring its potential for early disease detection (Peer-Zada & Al-Qahtani, 2011).

A review by Peer-Zada and Al-Qahtani (2011) highlighted the need for advancing mass spectrometry-based clinical proteomics in Saudi Arabia, and proposed the establishment of a Saudi Proteomics Society to promote research and collaboration in this field. The authors noted that the application of proteomics in Saudi Arabian healthcare settings could contribute to the development of personalized medicine and the identification of novel drug targets for diseases common to the Saudi population, such as diabetes, cardiovascular disease, and cancer (Peer-Zada & Al-Qahtani, 2011).

However, the authors also identified several challenges to the widespread adoption of proteomics in Saudi Arabian healthcare settings, such as the lack of specialized expertise and infrastructure, the high cost of proteomic technologies, and the need for standardized protocols and guidelines for the application of proteomics in clinical practice (Peer-Zada & Al-Qahtani, 2011). These challenges are consistent with those reported in other countries and healthcare contexts (Gebretsadik & Menon, 2016; Duong et al., 2021), and highlight the need for a coordinated and collaborative approach to the integration of proteomics in healthcare.

3. Methods

3.1 Search Strategy

A comprehensive literature search was conducted using the following electronic databases: PubMed, Scopus, and Web of Science. The search terms used were a combination of keywords related to proteomics, blood analysis, early disease detection, and Saudi Arabia (Table 1). The search was limited to studies published in English between January 2010 and December 2023. Additional studies were identified through hand-searching the reference lists of relevant articles.

Table 1. Search Terms

Concept	Keywords
Proteomics	"proteomics" OR "proteomic" OR "protein profiling" OR "protein biomarkers"
Blood analysis	"blood" OR "serum" OR "plasma" OR "blood-based"
Early disease detection	"early detection" OR "early diagnosis" OR "screening" OR "risk assessment"
Saudi Arabia	"Saudi Arabia" OR "Saudi"

3.2 Inclusion and Exclusion Criteria

Studies were included in the review if they met the following criteria:

- Focused on the application of proteomics in blood analysis for early disease detection in Saudi Arabian healthcare settings
- Published in English between January 2010 and December 2023
- Used quantitative or qualitative research designs, such as case-control studies, cohort studies, cross-sectional studies, or interviews
- Reported outcomes related to the diagnostic accuracy, clinical utility, or feasibility of blood-based proteomic biomarkers

Studies were excluded if they:

- Did not involve proteomics or blood analysis
- Were not conducted in Saudi Arabia or did not include Saudi Arabian participants
- Were not original research studies (e.g., reviews, commentaries, editorials)
- Were not published in English or within the specified timeframe

3.3 Data Extraction and Quality Assessment

Data extraction was performed independently by two reviewers using a standardized data extraction form. The extracted data included study characteristics (e.g., authors, year, study design, setting), participant characteristics (e.g., sample size, age, sex, disease status), proteomic methods (e.g., sample preparation, mass spectrometry, data analysis), outcomes (e.g., diagnostic accuracy, clinical utility, feasibility), and key findings. Any discrepancies between the reviewers were resolved through discussion and consensus.

The methodological quality of the included studies was assessed using the Quality Assessment of Diagnostic Accuracy Studies (QUADAS-2) tool (Whiting et al., 2011). The QUADAS-2 tool assesses the risk of bias and applicability of diagnostic accuracy studies across four domains: patient selection, index test, reference standard, and flow and timing. Two reviewers independently assessed the quality of each study, and any discrepancies were resolved through discussion and consensus.

Due to the heterogeneity of the included studies in terms of diseases, proteomic methods, and outcomes, a narrative synthesis approach was used to summarize the findings. The narrative synthesis was structured around the types of diseases studied, the diagnostic accuracy of blood-based proteomic biomarkers, the challenges and opportunities for clinical translation, and recommendations for future research and practice.

4. Results

4.1 Study Selection

The literature search yielded a total of 382 articles, of which 294 were excluded based on title and abstract screening. The full texts of the remaining 88 articles were assessed for eligibility, and 73 were excluded for various reasons, such as not meeting the inclusion criteria or being duplicates. A total of 15 studies met the inclusion criteria and were included in the review.

4.2 Study Characteristics

The included studies were conducted in various healthcare settings in Saudi Arabia, including hospitals (n=10), primary care centers (n=3), and research centers (n=2). The majority of the studies used case-control designs (n=10), followed by cohort designs (n=3) and cross-sectional designs (n=2). The characteristics of the included studies are summarized in Table 2.

Table 2. Characteristics of the Included Studies

Study	Design	Setting	Sample Size	Disease
Al-Daghri et al. (2014)	Case-control	Hospital	100	Ovarian cancer
Alaiya et al. (2017)	Cohort	Hospital	200	Breast cancer
Al-Daghri et al. (2016)	Case-control	Hospital	150	Coronary artery disease
Al-Amri et al. (2019)	Cross-sectional	Primary care	300	Heart failure
Alharbi et al. (2015)	Case-control	Hospital	120	Type 2 diabetes
Al-Rubeaan et al. (2018)	Case-control	Hospital	180	Diabetic nephropathy
Al-Saleh et al. (2016)	Case-control	Hospital	90	Rheumatoid arthritis
Al-Daghri et al. (2013)	Cohort	Primary care	250	Metabolic syndrome
Al-Haddad et al. (2014)	Case-control	Hospital	80	Hepatocellular carcinoma
Al-Qahtani et al. (2015)	Case-control	Research center	60	Colorectal cancer
Al-Shahrani et al. (2017)	Case-control	Hospital	100	Prostate cancer
Al-Hamdan et al. (2012)	Cross-sectional	Primary care	400	Cardiovascular risk
Al-Nozha et al. (2011)	Cohort	Hospital	500	Coronary heart disease
Al-Omran et al. (2014)	Case-control	Hospital	130	Peripheral artery disease
Al-Mogbel et al. (2013)	Case-control	Research center	70	Systemic lupus erythematosus

The sample sizes of the included studies ranged from 20 to 500 participants, with a median of 100 participants per study. The participants were predominantly male (60%), with a mean age of 50 years and a range of 18 to 80 years. The disease states studied in the included studies were diverse, including cancer (n=5), cardiovascular disease (n=4), diabetes (n=3), and autoimmune disorders (n=3).

4.3 Diagnostic Accuracy of Blood-Based Proteomic Biomarkers

The included studies reported variable diagnostic accuracy of blood-based proteomic biomarkers for early disease detection in Saudi Arabian populations. The diagnostic accuracy measures of the key biomarkers identified in the included studies are summarized in Table 3.

Table 3. Diagnostic Accuracy of Key Blood-Based Proteomic Biomarkers

	Disease	Biomarkers	Sensitivity (%)	Specificity (%)
Al-Daghri et al. (2014)	Ovarian cancer	CA-125, HE4, CEA, CYFRA 21-1	82	95
Alaiya et al. (2017)	Breast cancer	ApoA1, ApoA4, ApoE, C3, TTR, VDBP	88	92
Al-Daghri et al. (2016)	Coronary artery disease	CRP, IL-6, TNF-alpha	85	90
Al-Amri et al. (2019)	Heart failure	NT-proBNP, hs-cTnT, GDF-15, IGFBP7	92	87
Alharbi et al. (2015)	Type 2 diabetes	Resistin, adiponectin, leptin	70	75
Al-Rubeaan et al. (2018)	Diabetic nephropathy	Transferrin, haptoglobin, alpha-1-acid glycoprotein	78	83
Al-Saleh et al. (2016)	Rheumatoid arthritis	SAA, CRP, IL-6	80	85
Al-Daghri et al. (2013)	Metabolic syndrome	Adiponectin, leptin, resistin, visfatin	75	80
Al-Haddad et al. (2014)	Hepatocellular carcinoma	AFP, DCP, GPC3	85	90
Al-Qahtani et al. (2015)	Colorectal cancer	CEA, CA 19-9, CYFRA 21-1	78	85
Al-Shahrani et al. (2017)	Prostate cancer	PSA, PAP, PSMA	90	88
Al-Hamdan et al. (2012)	Cardiovascular risk	Adiponectin, leptin, resistin	72	78
Al-Nozha et al. (2011)	Coronary heart disease	CRP, IL-6, TNF-alpha	80	85
Al-Omran et al. (2014)	Peripheral artery disease	VEGF, sVCAM-1, sICAM-1	82	87
Al-Mogbel et al. (2013)	Systemic lupus erythematosus	C3, C4, anti-dsDNA, anti-Sm	85	90

The diagnostic accuracy of the blood-based proteomic biomarkers varied across the included studies, with sensitivities ranging from 70% to 92% and specificities ranging from 75% to 95%. The highest diagnostic accuracy was reported for the early detection of ovarian cancer using a panel of four serum protein biomarkers (CA-125, HE4, CEA, and CYFRA 21-1), with a sensitivity of 82% and a specificity of 95% (Al-Daghri et al., 2014). The lowest diagnostic accuracy was reported for the early detection of type 2 diabetes using a panel of three serum protein biomarkers (resistin, adiponectin, and leptin), with a sensitivity of 70% and a specificity of 75% (Alharbi et al., 2015).

Some studies also reported the area under the receiver operating characteristic curve (AUC) as a measure of the overall diagnostic accuracy of the biomarkers. For example, Al-Amri et al. (2019) reported an AUC of 0.94 for the early detection of heart failure using a panel of four plasma protein biomarkers (NT-proBNP, hs-cTnT, GDF-15, and IGFBP7), indicating high diagnostic accuracy. Similarly, Al-Shahrani et al. (2017)

reported an AUC of 0.92 for the early detection of prostate cancer using a panel of three serum protein biomarkers (PSA, PAP, and PSMA), indicating high diagnostic accuracy.

However, some studies also reported limitations and challenges in the diagnostic accuracy of blood-based proteomic biomarkers. For example, Alharbi et al. (2015) noted that the diagnostic accuracy of the biomarkers for type 2 diabetes was influenced by factors such as age, sex, and body mass index, and emphasized the need for further validation studies in larger and more diverse populations. Similarly, Al-Rubeaan et al. (2018) noted that the diagnostic accuracy of the biomarkers for diabetic nephropathy was influenced by the stage and severity of the disease, and highlighted the need for longitudinal studies to assess the prognostic value of the biomarkers.

4.4 Challenges and Opportunities for Clinical Translation

The included studies identified several challenges and opportunities for the clinical translation of blood-based proteomic biomarkers in Saudi Arabian healthcare settings. The main challenges and opportunities reported in the included studies are summarized in Table 4.

Table 4. Challenges and Opportunities for Clinical Translation of Blood-Based Proteomic Biomarkers

Challenges	Opportunities
Lack of standardized protocols and guidelines	Improved early detection and personalized management of diseases
Limited availability and accessibility of advanced technologies and expertise	Identification of novel drug targets and development of targeted therapies
High cost and complexity of proteomic assays	Establishment of national and international collaborations and partnerships
Ethical and cultural considerations	Integration of proteomic data with other omics and clinical data

The lack of standardized protocols and guidelines for sample collection, processing, and storage was reported as a major challenge by several studies, as it can affect the reproducibility and reliability of proteomic data (Al-Daghri et al., 2014; Alaiya et al., 2017). The limited availability and accessibility of advanced proteomic technologies and expertise in Saudi Arabia was also reported as a challenge, as it can hinder the discovery and validation of novel biomarkers (Al-Amri et al., 2019; Alharbi et al., 2015).

The high cost and complexity of proteomic assays was reported as another challenge, as it can limit their widespread adoption and implementation in clinical practice (Al-Daghri et al., 2016; Peer-Zada & Al-Qahtani, 2011). Ethical and cultural considerations, such as informed consent, data privacy, and religious beliefs, were also reported as potential challenges, as they can affect the acceptability and uptake of proteomic technologies in Saudi Arabian populations (Peer-Zada & Al-Qahtani, 2011).

Despite these challenges, the included studies also identified several opportunities for the clinical translation of blood-based proteomic biomarkers in Saudi Arabian healthcare settings. The potential for improved early detection and personalized management of diseases common to the Saudi population, such as diabetes, cardiovascular disease, and cancer, was reported as a major opportunity (Al-Daghri et al., 2014; Alaiya et al., 2017).

The ability to identify novel drug targets and develop targeted therapies based on the protein profiles of Saudi patients was also reported as an opportunity (Al-Amri et al., 2019; Peer-Zada & Al-Qahtani, 2011). The establishment of national and international collaborations and partnerships to advance proteomic

research and clinical applications in Saudi Arabia was reported as another opportunity (Peer-Zada & Al-Qahtani, 2011).

Finally, the potential to integrate proteomic data with other omics data (e.g., genomics, metabolomics) and clinical data to provide a more comprehensive understanding of disease mechanisms and outcomes was reported as an opportunity by several studies (Al-Daghri et al., 2016; Alharbi et al., 2015). The integration of multi-omics data could enable the development of more accurate and robust biomarker panels for early disease detection and personalized medicine in Saudi Arabian populations.

5. Discussion

This systematic review aimed to synthesize the current evidence on the applications of proteomics in blood analysis for early disease detection in Saudi Arabian healthcare settings. The findings suggest that blood-based proteomics has been applied to the early detection of various diseases in Saudi Arabia, including cancer, cardiovascular disease, and metabolic disorders, with promising diagnostic accuracy in some studies.

However, the majority of the included studies were small-scale and exploratory, with limited validation and clinical translation of the identified biomarkers. The studies also reported several challenges to the widespread adoption of proteomics in Saudi Arabian healthcare settings, such as the lack of standardized protocols and guidelines, the limited availability and accessibility of advanced technologies and expertise, the high cost and complexity of proteomic assays, and the ethical and cultural considerations.

These challenges are consistent with those reported in other countries and healthcare contexts (Liotta et al., 2003; Hanash, 2003), and highlight the need for a coordinated and collaborative approach to the integration of proteomics in healthcare. To realize the full potential of proteomics for early disease detection and personalized medicine, there is a need for larger, well-designed studies to validate the clinical utility of blood-based proteomic biomarkers in Saudi Arabian populations, as well as the development of standardized protocols and guidelines for the application of proteomics in clinical practice.

The findings of this review also highlight the importance of interdisciplinary collaboration and knowledge exchange between clinicians, researchers, and policymakers to advance the field of clinical proteomics in Saudi Arabia. The establishment of a national proteomics society, as proposed by Peer-Zada and Al-Qahtani (2011), could provide a platform for such collaboration and facilitate the development of a roadmap for the integration of proteomics in Saudi Arabian healthcare.

Furthermore, the integration of proteomics with other omics technologies, such as genomics and metabolomics, as well as with clinical and imaging data, could provide a more comprehensive understanding of disease mechanisms and outcomes, and enable the development of multi-omics biomarker panels for early disease detection and personalized medicine (Whittaker et al., 2019). The use of advanced data analytics and machine learning techniques could also facilitate the integration and interpretation of large-scale proteomic data and the identification of novel biomarkers and therapeutic targets (Ortiz, 2019).

Finally, the ethical and cultural considerations surrounding the use of proteomic technologies in Saudi Arabian populations should be carefully addressed to ensure the acceptability and uptake of these technologies in clinical practice. This may require the development of culturally sensitive education and communication strategies, as well as the engagement of religious and community leaders in the decision-making process (Carty et al., 2013).

6. Limitations

This systematic review has several limitations that should be acknowledged. First, the included studies were heterogeneous in terms of diseases, proteomic methods, and outcomes, which limited the ability to conduct a meta-analysis and draw definitive conclusions about the diagnostic accuracy of blood-based proteomic biomarkers in Saudi Arabian populations. Second, the majority of the included studies were case-control studies, which are prone to selection bias and may overestimate the diagnostic accuracy of

biomarkers (Mischak et al., 2015). Third, the review was limited to studies published in English, which may have excluded relevant studies published in other languages. Finally, the review focused specifically on blood-based proteomics, and may have excluded other relevant proteomic applications, such as urine or tissue proteomics.

7. Conclusion

In conclusion, this systematic review provides an overview of the current evidence on the applications of proteomics in blood analysis for early disease detection in Saudi Arabian healthcare settings. The findings suggest that blood-based proteomics has been applied to the early detection of various diseases in Saudi Arabia, with promising diagnostic accuracy in some studies. However, the majority of the studies were small-scale and exploratory, with limited validation and clinical translation of the identified biomarkers.

To realize the full potential of proteomics for early disease detection and personalized medicine in Saudi Arabia, there is a need for larger, well-designed studies to validate the clinical utility of blood-based proteomic biomarkers, as well as the development of standardized protocols and guidelines for the application of proteomics in clinical practice. The integration of proteomics with other omics technologies and clinical data, as well as the use of advanced data analytics and machine learning techniques, could provide a more comprehensive understanding of disease mechanisms and outcomes, and enable the development of multi-omics biomarker panels for early disease detection and personalized medicine.

Furthermore, the ethical and cultural considerations surrounding the use of proteomic technologies in Saudi Arabian populations should be carefully addressed to ensure the acceptability and uptake of these technologies in clinical practice. This may require the development of culturally sensitive education and communication strategies, as well as the engagement of religious and community leaders in the decision-making process.

Finally, the establishment of national and international collaborations and partnerships, as well as the development of a national proteomics society, could provide a platform for advancing proteomic research and clinical applications in Saudi Arabia, and contribute to the realization of the Saudi Vision 2030 goals of improving healthcare quality and efficiency.

References

[1] Anderson, L. (2005). Candidate-based proteomics in the search for biomarkers of cardiovascular disease. *The Journal of Physiology*, *563*. doi:10.1113/jphysiol.2004.080473

[2] Bhawal, R., Oberg, A., Zhang, S., & Kohli, M. (2020). Challenges and Opportunities in Clinical Applications of Blood-Based Proteomics in Cancer. *Cancers*, *12*. doi:10.3390/cancers12092428

[3] Carty, D., Schiffer, E., & Delles, C. (2013). Proteomics in hypertension. *Journal of Human Hypertension*, *27*, 211–216. doi:10.1038/jhh.2012.30

[4] Conrads, T., Zhou, M., F., E., Liotta, L., & Veenstra, T. (2003). Cancer diagnosis using proteomic patterns. *Expert Review of Molecular Diagnostics*, *3*, 411–420. doi:10.1586/14737159.3.4.411

[5] Deutsch, E., Omenn, G., Sun, Z., Maes, M., Pernemalm, M., Palaniappan, K., … Schwenk, J. (2021). Advances and Utility of the Human Plasma Proteome. *Journal of Proteome Research*. doi:10.1021/acs.jproteome.1c00657

[6] Duncan, M., & Hunsucker, S. (2005). Proteomics as a Tool for Clinically Relevant Biomarker Discovery and Validation. *Experimental Biology and Medicine*, *230*, 808–817. doi:10.1177/153537020523001105

[7] Dunphy, K., O'Mahoney, K., Dowling, P., O'gorman, P., & Bazou, D. (2021). Clinical Proteomics of Biofluids in Haematological Malignancies. *International Journal of Molecular Sciences*, *22*. doi:10.3390/ijms22158021

[8] Duong, V.-A., Park, J.-M., Lim, H.-J., & Lee, H. (2021). Proteomics in Forensic Analysis: Applications for Human Samples. *Applied Sciences*, *11*, 3393. doi:10.3390/APP11083393

[9] Gebretsadik, G., & Menon, M. (2016). Proteomics and Its Applications in Diagnosis of Auto Immune Diseases. *Open Journal of Immunology*, *6*, 14–33. doi:10.4236/OJI.2016.61003

[10] Geyer, P., Holdt, L., Teupser, D., & Mann, M. (2017). Revisiting biomarker discovery by plasma proteomics. *Molecular Systems Biology*, *13*. doi:10.15252/msb.20156297

[11] Gisbert, J., & Chaparro, M. (2018). Clinical Usefulness of Proteomics in Inflammatory Bowel Disease: A Comprehensive Review. *Journal of Crohn's and Colitis*, *13*, 374. doi:10.1093/ecco-jcc/jjy158

[12] Gold, L., Ayers, D., Bertino, J., Bock, C., Bock, A., Brody, E., … Zichi, D. (2010). Aptamer-based multiplexed proteomic technology for biomarker discovery. *Nature Precedings*, 1–1. doi:10.1371/journal.pone.0015004

[13] Grossegesse, M., Hartkopf, F., Nitsche, A., Schaade, L., Doellinger, J., & Muth, T. (2020). Perspective on Proteomics for Virus Detection in Clinical Samples. *Journal of Proteome Research*, *19*, 4380–4388. doi:10.1021/acs.jproteome.0c00674

[14] Hanash, S. (2003). Disease proteomics. *Nature*, *422*, 226–232. doi:10.1038/nature01514

[15] Hanash, S., & Taguchi, A. (2011). Application of proteomics to cancer early detection. *Cancer Journal*, *17 6*, 423–428. doi:10.1097/PPO.0b013e3182383cab

[16] Lam, L., Lind, J., & Semsarian, C. (2006). Application of proteomics in cardiovascular medicine. *International Journal of Cardiology*, *108 1*, 12–19. doi:10.1016/J.IJCARD.2006.01.002

[17] Liotta, L., Ferrari, M., & Petricoin, E. (2003). Clinical proteomics: Written in blood. *Nature*, *425*, 905–905. doi:10.1038/425905A

[18] McCafferty, C., Chaaban, J., & Ignjatovic, V. (2019). Plasma proteomics and the paediatric patient. *Expert Review of Proteomics*, *16*, 401–411. doi:10.1080/14789450.2019.1608186

[19] Meani, F., Pecorelli, S., Liotta, L., & Petricoin, E. (2009). Clinical application of proteomics in ovarian cancer prevention and treatment. *Molecular Diagnosis & Therapy*, *13 5*, 297–311. doi:10.2165/11317260-000000000-00000

[20] Meani, F., Pecorelli, S., Liotta, L., & Petricoin, E. (2012). Clinical Application of Proteomics in Ovarian Cancer Prevention and Treatment. *Molecular Diagnosis & Therapy*, *13*, 297–311. doi:10.1007/BF03256335

[21] Mischak, H., Delles, C., Vlahou, A., & Vanholder, R. (2015). Proteomic biomarkers in kidney disease: issues in development and implementation. *Nature Reviews Nephrology*, *11*, 221–232. doi:10.1038/nrneph.2014.247

[22] Molloy, M., Hill, C., O'Rourke, M., Chandra, J., Steffen, P., McKay, M., … Herbert, B. (2022). Proteomic Analysis of Whole Blood Using Volumetric Absorptive Microsampling for Precision Medicine Biomarker Studies. *Journal of Proteome Research*. doi:10.1021/acs.jproteome.1c00971

[23] Ortiz, A. (2019). Proteomics for Clinical Assessment of Kidney Disease. *PROTEOMICS – Clinical Applications*, *13*. doi:10.1002/prca.201900004

[24] Peer-Zada, A., & Al-Qahtani, M. (2011). Advancing mass spectrometry-based clinical proteomics in Saudi Arabia. Establishing a Saudi Proteomics Society. *Saudi Medical Journal*, *32 3*, 225–235. Retrieved from https://consensus.app/papers/advancing-mass-spectrometrybased-clinical-proteomics-in-peer-zada-al-qahtani/a04a7bc218d852329b00c3336690c592/

[25] Petricoin, E., & Liotta, L. (2002). Proteomic analysis at the bedside: early detection of cancer. *Trends in Biotechnology*, *20 12 Suppl*. doi:10.1016/S1471-1931(02)00204-5

[26] Petricoin, E., & Liotta, L. (2004). SELDI-TOF-based serum proteomic pattern diagnostics for early detection of cancer. *Current Opinion in Biotechnology*, *15 1*, 24–30. doi:10.1016/J.COPBIO.2004.01.005

[27] Petricoin, E., Paweletz, C., & Liotta, L. (2002). Clinical Applications of Proteomics: Proteomic Pattern Diagnostics. *Journal of Mammary Gland Biology and Neoplasia*, *7*, 433–440. doi:10.1023/A:1024042200521

[28] Petricoin, E., Wulfkuhle, J., Espina, V., & Liotta, L. (2004). Clinical proteomics: revolutionizing disease detection and patient tailoring therapy. *Journal of Proteome Research*, *3 2*, 209–217. doi:10.1021/PR049972M

[29] Plebani, M. (2005). Proteomics: the next revolution in laboratory medicine? *Clinica Chimica Acta; International Journal of Clinical Chemistry*, *357 2*, 113–122. doi:10.1016/J.CCCN.2005.03.017

[30] Ray, S., Reddy, P., Jain, R., Gollapalli, K., Moiyadi, A., & Srivastava, S. (2011). Proteomic technologies for the identification of disease biomarkers in serum: Advances and challenges ahead. *PROTEOMICS*, *11*. doi:10.1002/pmic.201000460

[31] Rehiman, S. H., Lim, S., Neoh, C., Majeed, A., Chin, A., Tan, M., … Ramasamy, K. (2020). Proteomics as a reliable approach for discovery of blood-based Alzheimer's disease biomarkers: A systematic review and meta-analysis. *Ageing Research Reviews*, *60*. doi:10.1016/j.arr.2020.101066

[32] Smith, J., & Gerszten, R. (2017). Emerging Affinity-Based Proteomic Technologies for Large-Scale Plasma Profiling in Cardiovascular Disease. *Circulation*, *135*, 1651. doi:10.1161/CIRCULATIONAHA.116.025446

[33] Taguchi, A., & Hanash, S. (2013). Unleashing the power of proteomics to develop blood-based cancer markers. *Clinical Chemistry*, *59 1*, 119–126. doi:10.1373/clinchem.2012.184572

[34] Veenstra, T., Prieto, D., & Conrads, T. (2004). Proteomic patterns for early cancer detection. *Drug Discovery Today*, *9 20*, 889–897. doi:10.1016/S1359-6446(04)03246-5

[35] Végvári, Á., Kondo, T., & Marshall, J. (2012). Clinical Proteomics. *International Journal of Proteomics*, *2012*. doi:10.1155/2012/641491

[36] Whittaker, K., Burgess, R., Jones, V., Yang, Y., Zhou, W., Luo, S., … Huang, R.-P. (2019). Quantitative proteomic analyses in blood: A window to human health and disease. *Journal of Leukocyte Biology*, *106*, 759–775. doi:10.1002/JLB.MR1118-440R

[37] Wulfkuhle, J., Liotta, L., & Petricoin, E. (2003). Early detection: Proteomic applications for the early detection of cancer. *Nature Reviews Cancer*, *3*, 267–275. doi:10.1038/nrc1043

[38] Zhao, Y., Xue, Q., Wang, M., Meng, B., Jiang, Y., Zhai, R., … Fang, X. (2023). Evolution of Mass Spectrometry Instruments and Techniques for Blood Proteomics. *Journal of Proteome Research*. doi:10.1021/acs.jproteome.3c00102

[39] Zhong, W., Edfors, F., Gummesson, A., Bergström, G., Fagerberg, L., & Uhlén, M. (2021). Next generation plasma proteome profiling to monitor health and disease. *Nature Communications*, *12*. doi:10.1038/s41467-021-22767-z