Society of Medical Education & Research

2023, Volume 3, Issue 2, Page No: 45-64
ISSN: 3108-4826

Journal of Medical Sciences and Interdisciplinary Research

Nutritional Proteomics: A Pathway to Understanding and Optimizing Human Health

Hala Salim Sonbol[1*]

[1]Department of Biochemistry, Faculty of Science, King Abdulaziz University, Kingdom of Saudi Arabia, Jeddah, 21332, Saudi Arabia.

***E-mail** ✉ hsonbol@kau.edu.sa

Abstract

Proteomics is a branch of science that focuses on the study of proteins—how they are structured, function, and interact in living organisms. This review article explores the various aspects of proteomics and its broad applications in various research areas. It emphasizes the pivotal role the proteome plays in an organism, with changes influenced by its physiological state and environmental factors. Nutritional proteomics, or neuroproteomics, applies proteomic techniques to study how proteins interact with bioactive substances in food. Through approaches such as nutriproteomics and nutrigenomics, researchers gain deeper insights into the relationship between nutrients, proteins, and both the human proteome and genome. The paper discusses how proteome changes are associated with diseases, emphasizing the potential of nutritional proteomics in developing therapeutic strategies. This article highlights the ability of proteomics to identify biomarkers for various diseases and to uncover complex protein alterations associated with conditions such as cancer, cardiovascular diseases, neurodegenerative disorders, and infections. The review also explores how proteomic technologies contribute to drug discovery. Furthermore, it emphasizes the value of integrating multiple 'omics' disciplines to create a more comprehensive understanding of complex biological systems. In summary, the review highlights the significant promise of proteomic technologies in driving advancements in both scientific research and healthcare.

Keywords: Biomarkers, Proteomic, Omics, Nutritional proteomics, Disease-associated proteome

Introduction

Understanding nutritional proteomics

The proteome, which refers to the collection of proteins in an organism, is highly dynamic and varies in its function based on factors such as tissue type, the physiological condition of the organism, and environmental influences. This variability is crucial as the proteome provides essential information on both post-transcriptional and post-translational modifications, as well as gene expression patterns. Consequently, proteomics offers valuable insights into the adaptive capacity of an organism and serves as a snapshot of its current biological state [1].

Recent breakthroughs in omic technologies have made it possible to study the proteomes and peptidomes across various species. These advancements have led to the development of comprehensive protein databases that aid in protein identification, gene ontology analysis, and phylogenetic assessments through homology-based approaches [2].

Over the past decade, proteomics has undergone considerable advancement, solidifying its importance in numerous clinical and health-related applications. It has proven to be an indispensable tool in areas like food science, biomarker discovery, and drug target identification. Through the analysis of body fluids such as serum and urine, proteomic research has uncovered biomarkers linked to a wide range of diseases, including cancer, cardiovascular diseases, AIDS, and renal conditions [3].

Access this article online https://smerpub.com/

Received: 14 August 2023; **Accepted:** 28 November 2023

How to cite this article: Sonbol HS. Nutritional Proteomics: A Pathway to Understanding and Optimizing Human Health. J Med Sci Interdiscip Res. 2023;3(2):45-64. https://doi.org/10.51847/SnZlWLL5go

Nutritional proteomics, sometimes referred to as neuroproteomics, is the application of proteomic techniques to explore the relationship between nutrition and protein behavior. This interaction can take place in two main ways: first, by examining how nutrients influence protein expression, which is typically assessed through protein mapping; and second, by studying how nutrients induce post-translational modifications or engage with proteins through interactions with small molecules. Such interactions lead to changes in the protein's three-dimensional structure [4].

The convergence of nutritional science, genomics, and proteomics has led to the emergence of new disciplines like neuroproteomics and nutrigenomics. These fields focus on exploring how nutrients affect both the human proteome and the genome. Anticipated advancements in other omics disciplines, such as metabolomics, interactomics, and microbiomics, are expected to deepen our understanding of the biological underpinnings of nutrition [5].

Proteomics, as described by Carbonaro [6], is divided into six key categories: functional proteomics, expression proteomics, protein-protein interaction analysis, proteome mining, post-translational modification study, and structural proteomics [7]. Functional proteomics focuses on understanding how proteins work and interact, helping to reveal the molecular mechanisms behind cellular processes and uncover proteins that have yet to be studied. On the other hand, expression proteomics investigates changes in protein levels, analyzing both the quality and quantity of protein expression under various conditions. The study of protein-protein interactions involves mapping out the complex networks within cells using a combination of experimental methods like in vitro, in vivo, and computational techniques, which may incorporate machine learning and predictive modeling. Structural proteomics explores how proteins fold into their 3D structures, how they interact with each other, and their potential for therapeutic use. Post-translational modifications, which include processes such as phosphorylation and glycosylation, regulate a wide range of cellular activities, including protein stability, signaling, and subcellular localization. Finally, proteome mining helps to classify proteins based on their involvement in disease, their function, or specific protein domains, such as in chemical proteome mining **(Figure 1)** [6, 8-12].

In addition to its traditional applications, proteomics has expanded into new areas like neuroproteomics and foodomics, where it is used to explore the connections between diet and health. Proteomics-based methods have become essential tools in nutritional science, offering a deeper understanding of how different foods and dietary patterns contribute to disease development and overall health [13]. Nutriproteomics and foodomics leverage proteomics techniques to explore how nutrients, functional foods, and nutraceuticals impact protein activity and expression in both humans and animals. As the consumption of these dietary components increases, understanding their effects on health becomes increasingly important. Therefore, research in these areas focuses on identifying proteins with bioactive properties, discovering potential disease biomarkers, and evaluating the safety and efficacy of nutraceuticals [13].

This review article explores the various aspects of proteomics and its broad applications in different research areas. It emphasizes the pivotal role the proteome plays in an organism, with changes influenced by its physiological state and environmental factors.

Results and Discussion

Advancing nutritional science through proteomics

With the rise of omics technologies, including genomics, transcriptomics, proteomics, and metabolomics, the field of personalized medicine is evolving rapidly, allowing for highly precise molecular insights into individual health. While each of these technologies has contributed to medical progress, alone they are insufficient to fully unravel the complexities of many diseases. This has led to a growing trend of integrating multiple omics disciplines to gain a more holistic understanding of both normal biological processes and disease mechanisms [14].

As food consumption patterns change worldwide, there is an increasing consumer demand for transparency regarding the food they eat. This has led to a surge in interest in foodomics, a field that uses advanced omics tools to study the composition and health impacts of food [15]. Foodomics combines various techniques, including genomics, transcriptomics, proteomics, metabolomics, peptidomics, and epigenetics, to address issues related to food safety, quality, and traceability, and to identify new bioactive compounds that may have health benefits [16]. Among these, proteomics plays a central role in advancing our understanding of how food affects the body at the molecular level [17].

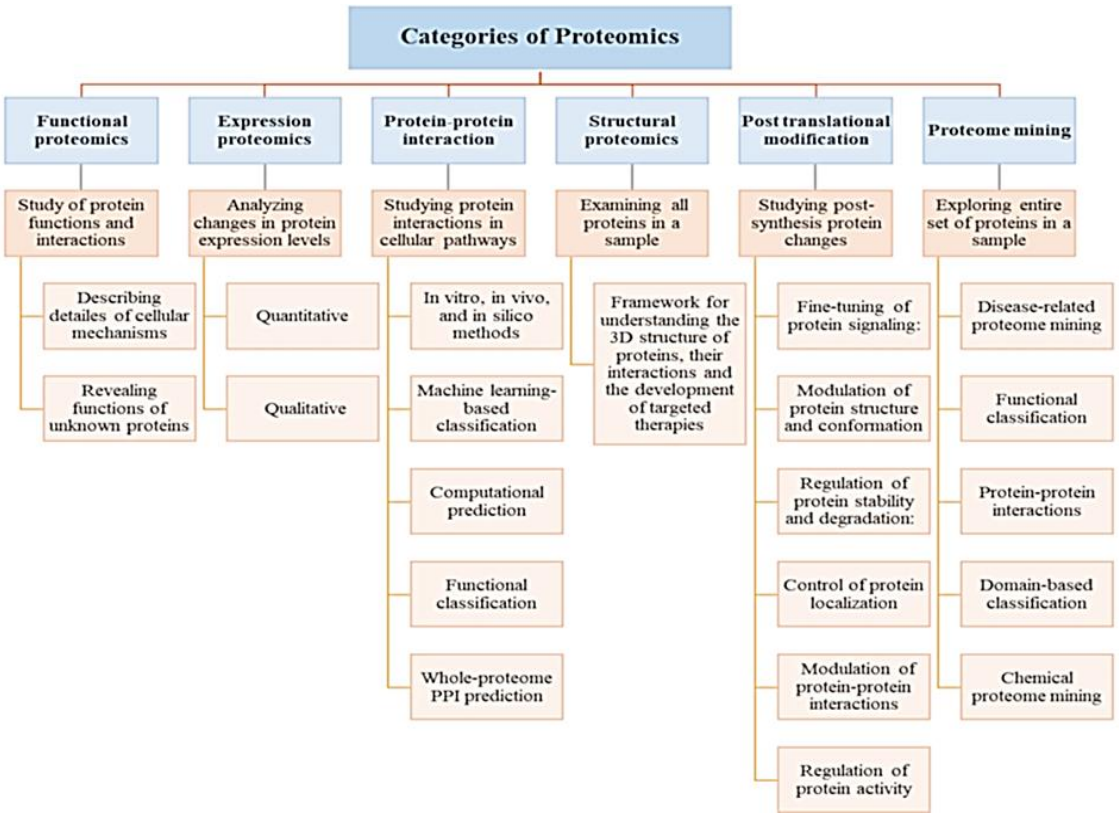

Figure 1. Proteomics categories; this diagram showcases the broad spectrum of proteomics research, highlighting different methodologies and areas of concentration; PPI refers to protein-protein interactions; the information presented in this figure is based on sources [6, 8-12].

Proteomics holds considerable promise for assessing food quality, which can be enhanced by optimizing food production techniques [18]. Food safety remains a critical health issue, as many individuals worldwide are affected by foodborne illnesses each year [19]. In addition, proteomics can be used to examine how different diets affect individuals at a molecular level. By analyzing changes in protein expression after dietary interventions, researchers can identify proteins or pathways influenced by specific dietary factors. This information can inform the development of personalized nutrition strategies aimed at managing diseases and optimizing health outcomes, based on individual protein expression profiles [20].

Proteomics is driven by several essential steps: (i) protein extraction, (ii) separation and quantification of proteins or peptides, (iii) protein identification, and (iv) data analysis and interpretation [8]. The initial phase involves isolating proteins from the sample to be studied [21]. Proteins are then separated using two-dimensional gel electrophoresis (2D-PAGE), a technique applied in both bottom-up and top-down proteomic methods [22].

The top-down approach, using mass spectrometry (MS), enables a detailed exploration of protein functions and modifications. The development of advanced mass spectrometers, coupled with liquid chromatography and sophisticated data analysis tools, has boosted the use of top-down proteomics. This technique allows for the identification of distinct protein variants, called proteoforms, which may exhibit notable differences in biological function. However, merely identifying these proteoforms may not provide sufficient insights into their biological roles. To address this, quantitative top-down MS methods have been developed, enabling researchers to study proteomes at the level of proteoforms rather than peptides [23].

In most proteomic studies, proteins are digested by proteases into smaller peptides, which are then analyzed by mass spectrometry (MS/MS). This approach involves matching the peptides' mass-to-charge ratios and predicted sequences to identify the proteins present. The

"bottom-up" proteomic method refers to this approach, where the peptides generated from protein digestion are matched to a protein database to identify their source [24].

Mass spectrometry (MS) is a powerful tool for protein characterization and the analysis of complex protein mixtures [25]. A variety of MS-based techniques have been developed for proteomic analysis, such as surface-enhanced laser desorption ionization (SELDI) [26], matrix-assisted laser desorption ionization (MALDI) [27] with time-of-flight (TOF) analyzers, and gas chromatography-mass spectrometry (GC-MS) or liquid chromatography-mass spectrometry (LC-MS). GC-MS and LC-MS are particularly valuable for separating complex mixtures, making them ideal for high-throughput proteomic analyses [28].

For successful proteomic analysis, the proteins being studied must be part of an accessible database. Commercial peptide fingerprint libraries, like "spectra bank," contain mass spectral data for various bacterial species, including those relevant to the food industry, with over 120 species cataloged [21]. Methods like high-performance liquid chromatography (HPLC) and mass spectrometry, coupled with liquid chromatography (MS/LC-MS), are commonly used to detect allergens and toxins in food [29].

The use of chromatographic techniques, such as ultra-high-performance liquid chromatography (UHPLC), has seen remarkable progress since the 21st century, particularly with improvements in mass spectrometry. These advances have made it possible to shift from traditional gel-based proteomics to chromatography-based methods, which can be label-free or label-assisted for protein quantification. The most common methods separate and quantify proteins at the peptide level. Typically, this involves denaturing proteins, digesting them enzymatically, and separating the resulting peptides using one- or two-dimensional liquid chromatography (2D-LC) [29].

Nutritional proteomics in disease prevention

Proteomics offers significant promise in the identification of disease biomarkers, which serve as biological indicators for the presence of specific diseases. Biomarkers can take various forms, with microRNAs, inflammatory markers, adipocytokines, oxidative stress, gut microbiota, nutrient levels, and blood cell profiles being some of the most commonly used types. Detecting these biomarkers early on is often associated with metabolic disorders or syndromes, thus highlighting the importance of identifying miRNAs as part of early diagnostic and preventative strategies. For example, biomarkers like microRNA, adipocyte-related proteins, oxidative stress markers, and various nutrients and microbiota are valuable in identifying obesity, a condition that warrants a comprehensive approach to prevention due to its broad impact across nations [30].

Advances in omic technologies have enhanced the identification of disease biomarkers and provided deeper insights into how diseases are influenced by specific nutrients [31]. Standard nutritional biomarkers, such as albumin, prealbumin, transferrin, and C-reactive protein (CRP), are commonly used; however, their reliability in representing true nutritional status has been questioned due to weak correlations with actual nutritional conditions [32]. Additionally, factors like inflammation, hydration status, and zinc deficiency can interfere with the accuracy of these biomarkers. Despite these challenges, nutritional biomarkers remain crucial tools in clinical settings, and ongoing research continues to explore new biomarker candidates through omic technologies. However, implementing omic-based biomarkers in personalized nutrition remains complex due to metabolic regulation intricacies, and technical and financial limitations continue to hinder their widespread application as simple, affordable tools for personalized nutrition [33]. The unreliability of current biomarkers underscores the need to discover highly specific and reliable markers for nutrition-related health assessments. To validate protein biomarkers in clinical practice, antibody-based methods such as enzyme-linked immunosorbent assays (ELISA) are often employed [34].

Personalized nutrition strategies that leverage nutritional proteomics allow for tailored dietary plans that address the unique nutritional needs of individuals, thus facilitating disease prevention and management. By integrating findings from nutritional proteomics with other omic approaches, researchers can design comprehensive, individualized nutrition strategies aimed at optimizing nutrient intake and preventing or managing diseases [35]. When it comes to managing diseases like cancer, nutritional proteomics can identify protein pathways affected by dietary factors, offering valuable insights into the design of interventions that improve patient outcomes and potentially control disease progression **(Figure 2)** [36].

Exploring disease-associated proteome changes

Proteins serve as intermediaries that link genetic and non-genetic risk factors to disease outcomes, providing essential insights into the biological mechanisms behind disease development. By correlating protein expression levels with genetic variants associated with risk alleles for common diseases, it is possible to uncover disease-related pathways, which could lead to the identification of novel drug targets and biomarkers for clinical applications [37]. Keijer *et al.* [38] have emphasized that personalized nutrition is becoming increasingly recognized as an effective strategy for improving health, optimizing diet, and preventing diet-related diseases. While omic technologies offer deep insights into metabolic processes, translating this knowledge into practical, affordable, and user-friendly personalized nutrition protocols remains challenging due to the complexity of metabolic regulation and the limitations of current technical and economic resources [38]. Proteomics, however, plays a crucial role in identifying potential biomarkers linked to disease progression. **Table 1** presents examples of proteins that are well-established as biomarkers in various human diseases.

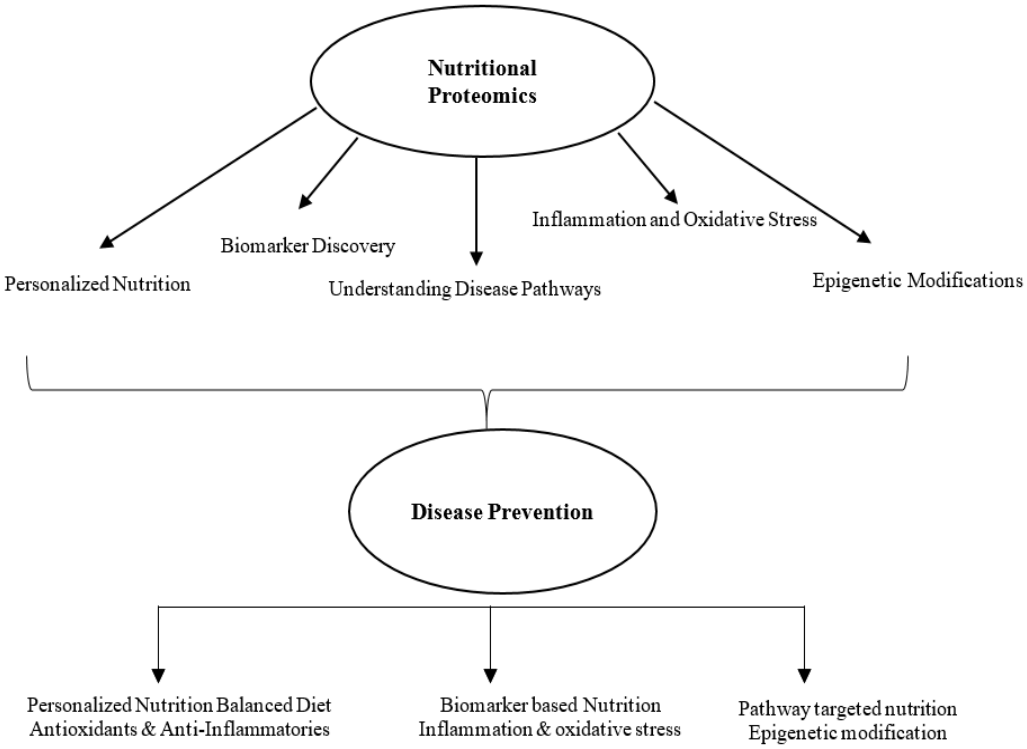

Figure 2. The intersection of nutritional proteomics and disease prevention

Table 1. Compilation of protein biomarkers in several human diseases

Protein potential biomarkers	Human disease condition	References
Hemoglobin A1c	Long-term glucose control in diabetes	[39]
Haptoglobin	Hemolytic anemia or other conditions involving red blood cell breakdown	[40]
CA 72-4	Gastric cancer	[41]
p53	Lung, colorectal, and ovarian cancers	[42]
Myoglobin	Signal muscle damage, such as in cases of heart attack or muscle injuries	[43]
Procalcitonin	The presence of bacterial infections	[44]
S100 Protein	Indicative of certain types of skin cancer, such as melanoma	[45]
Troponin	Diagnosing heart attacks	[46]
Cystatin C	Kidney function	[47]

Cystic fibrosis transmembrane conductance regulator	Cystic fibrosis	[48]
Bence jones protein	Multiple myeloma, a type of blood cancer	[49]
Prostate-specific antigen	Prostate cancer	[50]
Human epidermal growth factor receptor	Breast cancer	[51]
Brain natriuretic peptide N-terminal fragment of the prohormone	Heart failure	[52]

After the identification of biomarkers using mass spectrometry techniques, they must undergo additional bioinformatics analysis and be validated across different population groups [53].

Cancer

Proteomics has been instrumental in uncovering protein biomarkers that aid in the early detection of cancers, including breast cancer [54]. However, our understanding of the role dietary components play in cancer prevention remains limited. Changes in nutrient consumption involve the complex regulation of various protein networks, which include transcription factors, histone modifications, enzymes, translation regulators, receptors, and secreted proteins. Yet, conventional protein analysis methods are inadequate for fully quantifying and evaluating the complete set of proteins involved in cancer-related pathways [36].

Nutrigenetics investigates the impact of genetic variations on our body's response to nutrients and vice versa [55]. This knowledge enables a deeper integration of nutrition with personalized medicine, offering the potential for more tailored cancer treatments. Certain nutrients can activate mechanisms that inhibit cancer growth, targeting essential processes like apoptosis and angiogenesis, which are pivotal in cancer development [56].

Among various lifestyle factors, nutrition plays a critical role in the initiation, progression, and spread of cancer [57]. Research indicates that nutritional strategies, such as fasting alongside standard cancer treatments, can improve treatment outcomes. By applying genomics and nutrigenomics, scientists are unraveling the molecular pathways involved in fasting. Nutrigenomics can also uncover biomarkers that guide nutritional strategies in cancer therapy. This involves performing quantitative proteomic analyses on cancer cells and animal models to better understand these connections [57].

Researchers believe that incorporating nutritional approaches into clinical practice could enhance the effectiveness of chemotherapy and improve outcomes for cancer patients. Nutrigenomics explores the relationship between the nutrients we ingest and gene expression, offering insight into the molecular effects of dietary changes. Proteomics has not yet been fully leveraged to explore how nutrition affects cancer [57].

A study by Zhou *et al.* [58] proposed expanding cancer proteomic research, which could lead to the discovery of new cancer biomarkers and treatment strategies. They highlighted the importance of proteomic characterization to understand molecular abnormalities in cancers. Traditional cancer profiling methods have limitations, and Zhou *et al*. conducted a large-scale proteomic study involving 16 major human cancers. They analyzed 126 primary tumor samples, 94 adjacent normal tissues, and 12 normal tissues using advanced mass spectrometry techniques. Their findings identified 8,527 proteins across various cancers, including those affecting the brain, head and neck, breast, lung, and several other organ types.

This comprehensive analysis identified 2,458 tissue-specific proteins, providing valuable insights into the unique properties of each tissue type. They also discovered proteins common across all tissues and those specific to certain types of cancer. Among their findings were 1,139 proteins with potential therapeutic applications and 21 cancer/testis antigens, which could serve as targets for cancer treatments and diagnostic purposes [58].

While numerous laboratory studies have shown that specific nutrients may inhibit cancer, questions remain about whether these compounds possess pro-carcinogenic or anti-carcinogenic effects. Despite a significant number of preclinical and clinical studies, many of these trials have shown only marginally significant results [59].

To evaluate how nutrients affect cancer, it is important to explore how they interact with the hallmarks of cancer via their molecular mediators. The hallmark most notably influenced by nutrients is inflammation, which is driven by oxidative stress from reactive oxygen species [60].

Oral cancer can largely be prevented through maintaining good oral hygiene, avoiding tobacco and alcohol, and following a nutritious, balanced diet. Environmental exposure plays a significant role in the development of oral cancer, and these preventative measures can significantly reduce the risk of developing it [61]. Studies have shown that consuming a diet rich in fruits and vegetables lowers the risk of cancers of the oral cavity, head, and neck. This effect is especially marked in individuals who smoke or drink alcohol, as they are generally at a higher risk for oral cancer [62]. It is well-established that certain dietary components can act as triggers for cancer development. Furthermore, some research indicates that specific dietary patterns, such as the ketogenic diet, may help prevent normal cells from becoming cancerous, or even slow the progression and spread of existing tumors [63]. A pilot study employing label-free serum proteomics analyzed the serum protein profiles of 13 patients with oral squamous cell carcinoma and 12 healthy controls [64]. The study found that it was possible to differentiate between patients with oral squamous cell carcinoma and healthy individuals by examining their serum proteomic profiles [64].

Breast cancer remains one of the leading causes of mortality, with the number of cases reaching 1,960,681 and resulting in 17,708,600 disability-adjusted life years (DALYs) in 2017 [65, 66]. Nutrigenomics is believed to be crucial for preventing and detecting breast cancer at an early stage. By understanding how nutrition influences breast cancer risk, particularly in individuals with rare cases or genetic mutations, valuable insights could be gained for early intervention and treatment [67]. Extensive research on breast cancer spans multiple areas, including epidemiology, societal impact, and economic consequences. The connection between breast cancer and dietary habits is complex, with numerous interacting factors that do not always follow a linear pattern. Traditional studies in nutritional epidemiology have produced varied results, showing only a weak association between diet and breast cancer risk, except in the case of alcohol consumption. The diverse nature of breast cancer, both in terms of its biological characteristics and clinical presentation, is well-documented, and molecular and histological classifications have further contributed to our understanding of the disease [5].

Proteomic techniques have been utilized to identify proteins disrupted in breast cancer, offering valuable insights into the molecular processes that drive the development and spread of the disease [68]. Moreover, proteomic profiling has proven useful in discovering potential biomarkers that can aid in the diagnosis, prognosis, and treatment of breast cancer. These biomarkers play an essential role in distinguishing breast cancer patients from healthy individuals and predicting patient outcomes [68].

Breast cancer has been investigated in depth using proteomic analysis of formalin-fixed paraffin-embedded tissue samples, providing valuable insights into the molecular alterations linked to the disease. This analysis has proven useful for prognostic evaluations based on the tumor, node, and metastasis (TNM) staging system, helping predict disease outcomes more effectively [69]. In addition, the study of tear proteomes has been instrumental in comparing protein levels between breast cancer patients and healthy controls. This method has highlighted key molecular changes associated with the cancer, offering potential biomarkers for earlier detection and diagnosis [70].

Proteomic methods involving mass spectrometry, such as top-down, middle-down, and bottom-up approaches, complement traditional histological techniques by simultaneously analyzing multiple aspects of protein function, including expression, modifications, and interactions. Advanced mass spectrometry techniques like LC-MS/MS, MALDI-TOF MS, SELDI-TOF MS, MALDI-TOF/TOF MS, and MALDI MSI are used in conjunction with conventional pathology, enabling the detailed examination of protein expression patterns, modifications, and interactions between proteins. Identifying proteins with altered expressions is crucial for several applications in breast cancer research, including the discovery of new biomarkers, assembling panels for early diagnosis, distinguishing between breast cancer subtypes, investigating post-translational modifications and protein-protein interactions, providing insights into accurate diagnoses and prognosis, and understanding how these altered proteins contribute to the initiation, invasion, and resistance of tumors to treatments [68].

The role of natural substances like vitamins C, E, D, B, A, K, and selenium is increasingly recognized in cancer prevention [71]. These compounds are believed to play important roles in inhibiting cancer development. While they may not directly induce apoptosis in cancer cells, the impact of vitamins and other bioactive molecules, whether from food sources or synthesized drugs, is being explored through advanced oncological research. Deficiencies in these essential nutrients have been

associated with various cancers, and their genetic and biological influence is being studied for better insight into underlying mechanisms. Systems biology approaches are being applied to evaluate the optimal dosages of these micronutrients to maximize their potential benefits [72].

In summary, neuroproteomics has contributed significantly to understanding the molecular mechanisms driving breast cancer and has provided valuable information on potential biomarkers for early diagnosis. These advancements have the potential to improve treatment outcomes and reduce the overall impact of breast cancer [68].

Cardiovascular disease

Atherosclerotic cardiovascular disease (ASCVD) was once primarily seen as a health issue in developed countries, but it has increasingly become a global concern [73]. A major challenge in preventing coronary heart disease has been the difficulty in detecting early-stage atherosclerosis. Gaining insight into the changes in arterial protein networks during the early stages of the disease could potentially uncover new biomarkers for early diagnosis and provide more effective targets for treatment [74].

A study investigating proteins within human coronary and aortic tissues identified specific proteins, networks, and regulatory systems that were either unique to each artery or indicative of early-stage atherosclerosis. The findings demonstrated that the proteins uncovered through tissue proteomics could be utilized to develop plasma biomarker tests with clinical relevance. Notably, the study revealed significant differences in mitochondrial protein levels between coronary and aortic tissues, suggesting that coronary arteries have a greater capacity for aerobic metabolism. Additionally, the protein mass in mitochondria differed considerably between the two arterial types [74]. Advances in plasma proteomics, especially when combined with machine learning techniques, may open new pathways for improving risk stratification in ASCVD patients [75].

In another investigation, a group of researchers sought to enhance cardiovascular risk prediction by applying targeted plasma proteomics in primary prevention. The study compared the efficacy of a proteomic-based risk model against one based on traditional risk factors to predict cardiovascular events in the EPIC-Norfolk study cohort. The findings were further validated in the PLIC cohort. The research indicated that the proteomic model was more accurate than the clinical risk factor-based model in predicting cardiovascular events in a primary prevention setting. However, the researchers pointed out that further validation in larger primary prevention cohorts is necessary to determine the clinical utility of this model in preventing cardiovascular diseases [76].

Through a proteomic analysis identifying 85 key proteins associated with cardiovascular disease, the researchers identified distinct biomarkers linked to various cardiovascular outcomes. Specifically, they found eight biomarkers associated with ASCVD, 18 with heart failure (HF), 38 with all-cause mortality, and 35 with cardiovascular-related deaths. They accounted for potential confounding factors in their analysis. GDF15 emerged as a biomarker connected to all outcomes when considered alongside clinical factors [77].

Additionally, biomarkers like NT-proBNP, CRP, and leptin were linked to incident HF. In a broader multimarker model, proteins such as CLEC3B, AGP1, sRAGE, PMP2, UCMGP, KLKB1, IGFBP2, IGF1, leptin receptor, and cystatin-C were found to be associated with overall mortality rates [77].

These results highlight multiple new associations between protein biomarkers regulating metabolic and inflammatory processes and various cardiovascular outcomes. Using a high-throughput proteomic approach, the researchers were able to uncover new relationships between biomarkers and cardiovascular events, while also validating previously known genetic associations [77].

Neurodegenerative conditions

Neurodegenerative conditions are often diagnosed based on observable clinical symptoms and advanced brain imaging techniques. These conditions present a wide range of symptoms that reflect different underlying neurodegenerative processes, often varying from patient to patient. Research has revealed that distinct pathologies can lead to similar clinical manifestations, making precise diagnosis increasingly challenging [78]. Exploring these diseases at the molecular level can uncover key proteins and metabolites involved in cellular functions, which could then inform the development of therapies aimed at halting or reversing disease progression [78].

A hallmark of neurodegenerative diseases is the abnormal aggregation of proteins in the brain. Andrews *et al.* [78] employed pulse isotope labeling in vivo to track changes in protein turnover and abundance across

several mouse models of neurodegeneration. Their study revealed that in diseased tissue, protein turnover and repair are elevated, while in healthy aging mice, protein turnover slows down significantly [79]. The levels of proteins in the brain are controlled by their rate of synthesis and degradation, which are influenced by cellular machinery. By combining metabolic labeling with global proteomics, the researchers could measure both the synthesis and degradation of proteins in real time, allowing them to separate the effects of these two processes. The study found that increased protein turnover in certain models correlated with greater disease severity, offering a powerful method to investigate proteome dynamics and identify affected proteins in living animals [79].

Dementia, a prevalent condition in the elderly, currently lacks an effective cure. However, advancements in proteomics offer the potential for identifying brain proteome alterations that could provide insight into the mechanisms behind the disease and help identify biomarkers for diagnosis. Studies of the brains of individuals with Alzheimer's disease, Parkinson's disease dementia, frontotemporal dementia, and amyotrophic lateral sclerosis have confirmed previous findings and identified new proteins associated with these conditions [66].

Many dementias are classified as proteinopathies, conditions characterized by abnormal protein accumulation in the brain [66]. Proteomics provides a method for detecting these protein abnormalities, though challenges such as the complexity of the diseases, variability among patients, and limited access to high-quality brain tissue have hindered progress. Nevertheless, recent advances in mass spectrometry have allowed researchers to analyze the complete proteome of brain tissues or cells in a shorter timeframe, even when working with limited clinical samples [66, 80].

Parkinson's disease dementia (PDD) affects 2-3% of those over 65, while dementia with Lewy bodies (DLB) accounts for 15-20% of cases of late-onset dementia [81]. PDD patients typically experience mild memory loss and motor symptoms due to the buildup of Lewy bodies containing α-synuclein (SNCA) in the substantia nigra. The exact cause of PDD remains unclear, although it is believed to involve a complex interplay of genetic and environmental factors. Early-onset Parkinson's disease is rare but can be caused by specific genetic mutations [81]. Research into Parkinson's disease has focused on its molecular origins and clinical manifestations. High-throughput proteomic analysis of cerebrospinal fluid (CSF) has provided valuable insights into the disease's diversity [82]. Proteomic differences between idiopathic Parkinson's patients and healthy controls suggest increased neuroinflammation, possible neuroprotection through vasoactive compounds, and disturbances in iron metabolism and mitochondrial function. Proteomic profiling has also enabled the identification of distinct "endotypes," or subgroups of patients with different trajectories in cognitive and motor symptoms, correlating with known protein-based risk factors [82].

Alzheimer's disease, the most common form of dementia, is marked by the buildup of β-amyloid (Aβ) plaques and neurofibrillary tangles in the brain. Numerous quantitative proteomics studies on brain tissue, CSF, plasma, and animal models of Alzheimer's have contributed to a better understanding of the disease. Research on MS-based proteomics provided an overview of the process involved in identifying and validating potential biomarkers for Alzheimer's [83].

Proteomics is a technique used to study biological samples at the protein level, with the bottom-up approach being one of the most commonly employed methods. This technique combines liquid chromatography with tandem mass spectrometry to identify and quantify peptides derived from digested proteins. Recent progress in proteomics has allowed researchers to quantify over 2000 proteins, revealing important molecular changes in the brains of individuals with neurodegenerative diseases [84, 85]. Quantitative proteomics typically uses label-free data-dependent acquisition or isobaric multiplex labeling strategies, such as iTRAQ or TMT reagents [84].

Infectious diseases

Proteomic analysis has proven to be an essential approach in investigating the molecular changes that occur during infectious diseases, including viral infections such as HIV and hepatitis C, as well as bacterial infections like tuberculosis. Infectious diseases are responsible for about a quarter of global deaths, including major contributors such as HIV/AIDS, respiratory bacterial infections, and malaria [86].

The ability to assess and identify proteins involved in infectious diseases has greatly advanced due to proteomics, making it a powerful technique for understanding these conditions [87]. Environmental factors, particularly those resulting from infections, can significantly alter the proteomic landscape of organisms, tissues, and cells [87]. Proteomics plays a critical role in

studying the pathophysiology, causes, and progression of infectious diseases [87]. Furthermore, this technology is vital in identifying pathogens, tracking the emergence of new infectious agents, and examining their molecular behavior [88]. A key focus of proteomics is studying the interaction between hosts and pathogens, which is fundamental in understanding the complexities of infectious diseases [89].

The evolution of various scientific techniques in genetics, molecular biology, and imaging has greatly advanced microbiological research in recent decades. The increased use of mass spectrometry (MS) and proteomics has provided deeper insights into the molecular mechanisms of pathogen-host interactions and the biological underpinnings of infectious diseases [90]. Researchers have outlined how MS-based proteomics contributes to understanding the molecular features of viruses and bacteria, shedding light on their interactions with host organisms. Their work highlights how these proteomic techniques are supporting the development of diagnostics, treatments, and the integration of multi-omics approaches for a broader systems biology perspective on pathogen-host dynamics [91]. Numerous infectious diseases, including HIV/AIDS, tuberculosis, malaria, measles, and hepatitis, have been extensively studied using proteomics, and it is clear that a small set of pathogens are responsible for the majority of global infectious disease-related fatalities [87].

Proteomics is extensively used to evaluate how protein expression patterns shift in response to specific stimuli over defined periods, allowing for the determination of protein structures and their biological roles in governing cellular functions [87]. Unlike DNA microarray analysis, which examines gene expression, proteomics is often more effective in studying changes in protein patterns during specific conditions such as disease or pathogen presence. In studies of hepatitis, it has been found that serum from individuals with chronic hepatitis B (HBV) and hepatocellular carcinoma (HCC) exhibits significantly lower levels of apolipoprotein A1 (ApoA1) isoform and the C-terminal segment of complement factor C3, compared to healthy individuals, who show higher and more variable protein levels. Similarly, in HBV-infected mice, the liver proteins fatty acid-binding protein 5 and acyl-CoA-binding protein were found at elevated levels compared to normal mice. Techniques like 2D gel electrophoresis and immunoblotting have been employed to identify potential serum autoantibody biomarkers for chronic hepatitis C or HCV-related HCC. In addition, therapeutic interventions for HCV infection have led to noticeable shifts in various serum proteins, such as those involved in cytoskeletal organization, heat shock proteins (HSP70 and HSP60), molecular chaperones, metabolic enzymes like glutamine synthetase, and those regulating glycolysis and the urea cycle. Furthermore, proteomics has been pivotal in identifying novel biomarkers for diagnosing infections caused by Mycobacterium tuberculosis [87].

Proteomic techniques are also being applied to better understand pathogens that cause lower respiratory tract infections, which aids in discovering new vaccine targets and clarifying their role in disease mechanisms. For example, mass spectrometry-based methods like two-dimensional electrophoresis (2DE) and two-dimensional semipreparative electrophoresis (2DPE) have been used to identify potential vaccine candidates from *Haemophilus influenzae*, a gram-negative bacterium linked to otitis media, sinusitis, and pneumonia. Additionally, shotgun proteomics is proving valuable for studying the various lifecycle stages of the malaria parasite *Plasmodium falciparum*, contributing to a deeper understanding of the parasite's biology and lifecycle [87].

A newly developed multiplex proteomics assay has been introduced to assess the severity and prognosis of COVID-19. This method evaluates 50 peptides, which are a mix of both established and newly discovered COVID-19-related protein markers, using laboratory techniques like liquid chromatography and multiple reaction monitoring (LC-MRM). Researchers conducted two studies involving COVID-19 patients to confirm the assay's effectiveness. It was able to accurately differentiate between healthy individuals, and those with mild, moderate, or severe COVID-19 infections, capturing both infection characteristics and its severity [92].

Proteomic data has consistently proven its ability to classify and forecast COVID-19 outcomes effectively [93]. These datasets enable the quantification of multiple proteins in a single sample. Particularly in severe COVID-19 cases, proteomics has shown greater accuracy in predicting outcomes compared to traditional clinical tools such as the APACHE II score, the Charlson comorbidity index (CCI), and SOFA scores [94]. Furthermore, proteomics has played a crucial role in advancing the understanding of the host's antiviral response, revealing critical insights into COVID-19 pathology, including the involvement of the complement

cascade, coagulation system, and apoprotein function [95].

Nutritional proteomics in disease treatment

The role of nutrition in optimizing lifestyles for cancer prevention and therapy has been extensively studied. Researchers have explored various dietary interventions, such as calorie reduction, fasting, and carbohydrate limitation, and their effects on cancer biology. Additionally, proteomics has been pivotal in discovering cancer biomarkers and understanding how nutrition influences molecular mechanisms through nutrigenomics [57]. Interventions like fasting have broad implications on health and disease, potentially affecting cancer initiation, progression, and response to treatment. Many believe that combining fasting with standard cancer treatments could improve their effectiveness. Nutrigenomics offers significant potential by unveiling the molecular pathways triggered by fasting and identifying biomarkers that may guide nutritional interventions in cancer therapy. Quantitative proteomic studies involving fasting in animal models and tumor cells are essential in discovering these biomarkers, with the ultimate goal of using nutritional omics to assess tumor metabolic conditions and decide if fasting is an appropriate treatment for individual patients [57].

Proteomics technology has advanced considerably in the last decade, driven by high-throughput methods and enhanced data mining techniques. These innovations have led to large-scale datasets that enable the discovery of novel biomarkers essential for the early diagnosis and management of diseases [95]. In one study by Lee *et al*. [94], they explored how vitamin K deficiency affects the plasma proteins of 500 children in Nepal aged 6-8 years. By measuring lipids and the PIVKA-II protein, which is associated with a lack of vitamin K, they utilized mass spectrometry to identify key proteins linked to the deficiency. The study found that elevated levels of PIVKA-II (> 2 μg/L) were associated with higher concentrations of LDL, cholesterol, and triglycerides in the plasma. Out of 978 proteins studied, five showed a direct link to PIVKA-II levels, and seven exhibited differences between children with adequate and insufficient vitamin K. Proteins like coagulation factor-II, hemoglobin, and vascular endothelial cadherin were among those identified. The analysis revealed a strong correlation between hemoglobin subunits and enzymes protecting red blood cells from oxidative stress, hinting at connections between blood clotting, vascularization, and oxidative stress related to vitamin K deficiency. This study highlights the power of untargeted proteomics in studying blood clotting and red blood cell health under conditions of vitamin K deficiency [95].

The recent integration of high-throughput technologies, AI, and data mining in proteomics has greatly advanced the discovery of biomarkers and allowed for the analysis of complex clinical data. The future of proteomics promises to enhance our understanding of single-cell biology and revolutionize personalized medicine, offering exciting opportunities for research and healthcare improvements [96, 97].

Discovery of disease biomarkers

Biomarkers specific to diseases are categorized based on the type of information they provide: diagnostic, prognostic, or treatment-predictive [97]. Diagnostic biomarkers assist in identifying diseases or detecting them early on. Prognostic biomarkers help in forecasting the likelihood of disease recurrence, aggressiveness, and the patient's response to specific therapies [98]. In the realm of proteomics, the identification of biomarkers predicting weight loss in obese individuals has also gained attention [99]. A widely known biomarker, prostate-specific antigen (PSA), is frequently used in clinical settings. However, many cancers are often detected too late, resulting in poor outcomes due to limited treatment options. This delay stems from the labor-intensive and expensive process involved in detecting biomarkers. To address this, more efficient early detection methods need to be developed, ideally by integrating proteomic data from various platforms [100]. Monitoring alterations in protein expressions in biological samples such as blood, urine, or tissue can give crucial insights into disease onset, as proteins change during disease progression [99].

Recent studies underscore the potential of proteomic profiling in predicting weight loss, highlighting the significance of specific protein biomarkers [101]. Additionally, proteomics plays a vital role in identifying drug targets through techniques like chemical proteomics and protein interaction networks [3]. Combining proteomics with personalized nutrition holds significant promise in forecasting weight loss outcomes and improving overall health in individuals suffering from obesity [101]. After identifying biomarkers using mass spectrometry, it's necessary to perform a thorough bioinformatics analysis and validate these markers across diverse populations to ensure their accuracy [53].

Serum biomarkers

Beyond proteomics, other -omics technologies such as genomics, metabolomics, and transcriptomics are also being used to create personalized nutrition strategies for disease treatment [102]. A randomized trial involving 609 overweight and obese participants analyzed 263 proteins linked to inflammation and cardiovascular conditions before and after weight loss. It was found that 102 proteins were associated with baseline BMI, while 130 proteins were linked to weight loss. Among these, fibroblast growth factor 21 (FGF-21) levels were a strong predictor of weight loss. Interestingly, the type of diet did not significantly interact with baseline protein levels to affect weight loss. These results highlight the potential for using circulating proteins to understand obesity-related mechanisms, although their utility in predicting weight loss outcomes remains somewhat limited [101].

Proteomics also plays a critical role in identifying biomarkers for inflammatory bowel disease (IBD), which can aid in monitoring disease activity, mucosal healing, and cancer progression in IBD patients [102]. Biomarker discovery studies must account for variations in sample matrices, as these can influence the results [103].

A study employed SELDI-TOF-MS technology to analyze blood samples from patients with IBD, healthy individuals, and those with other inflammatory diseases. They identified four proteins—platelet factor 4 (PF4), haptoglobin 2 (Hp2), fibrinogen alpha chain (FIBA), and myeloid-related protein 8 (MRP8)—that could serve as indicators of disease activity in IBD [104].

In the context of COVID-19, proteomics has been instrumental in examining how nutritional biomarkers change before and after vaccination. In pre-vaccine cohorts, proteomic analysis revealed significant changes in serum proteins, with alpha-1-acid glycoproteins (AGPs) 1 and 2, C-reactive protein (CRP), and retinol-binding protein (RBP) levels increasing as the severity of COVID-19 worsened, while albumin, transthyretin (TTR), and serotransferrin (TF) levels decreased [104].

Incorporating personalized nutrition interventions along with oral or enteral supplements can help meet protein and energy requirements in COVID-19 patients while supporting the intestinal and lung microbiota. By improving diet and adding prebiotics or probiotics, these strategies can be combined with other treatments like vaccines to better manage COVID-19 [105]. Serum and plasma biomarkers also provide valuable information about how nutrition influences disease outcomes and help us understand the metabolic changes occurring in both infectious and non-infectious diseases [106].

Urinary biomarkers

Compared to plasma, urine serves as a less complicated sample, holding more than 1500 unique proteins [107]. What distinguishes urine is its consistent protein makeup, which remains relatively stable, unlike plasma or serum which can undergo degradation due to proteolysis during or after collection [107].

Proteomics offers a promising approach to uncover protein-related insights. Advanced techniques such as 2D-DIGE, MALDI-TOF/MS, and LC-MS/MS have been employed to study urine and serum from patients [108].

Neutrophil gelatinase-associated lipocalin (NGAL) and matrix metalloproteinase (MMP-9) have been highlighted as significant biomarkers in the urine of breast cancer patients. This discovery was made possible through the use of gelatin zymography [109]. In addition, MMP-9 and ADAM 12 have been identified as potential breast cancer biomarkers when subjected to zymography and immunoblotting with ADAM 12-specific antibodies [110].

Several biomarkers in urine have been associated with prostate cancer. Notably, stratifin, membrane metalloendopeptidase, Parkinson's protein 7, and tissue inhibitor of metalloproteinase 1 have been confirmed as reliable markers using LC-MS/MS, Western blotting, and selected reaction monitoring-MS [43]. Similarly, in a 2015 study, Li *et al.* [66] employed LC-MS/MS to validate osteopontin (SPP1), prothrombin (F2), pyridinoline, and deoxypyridinoline as prostate cancer biomarkers. Their research also revealed beta-2-microglobulin (B2-M), prostate cancer gene 3 (PGA3), and mucin 3 (MUC3) as dependable markers through quantitative iTRAQ, LC-MS/MS, and immunoblotting. Moreover, using 2D-DIGE-MS and immunoturbidimetry, they identified transferrin, alpha-1-microglobulin, and haptoglobin as potential prostate cancer biomarkers in urine [111].

Apolipoprotein D, insulin-like growth factor-binding protein 3, and ApoD levels were significantly increased in Alzheimer's patients compared to controls, as shown by enzyme-linked immunosorbent assays [112]. In addition, the α1-antitrypsin biomarker was found to be elevated in the urine of patients with diabetic nephropathy, with 2D-DIGE and ELISA methods used for its detection [113]. Pejcic *et al.* [112] also identified the ubiquitin ribosomal fusion protein (UbA52) as a

reliable biomarker through the SELDI technique. Furthermore, Dihazi *et al.* [113] applied SELDI to find that the processed form of ubiquitin was selectively absent in the urine of affected patients. The WNT1-inducible signaling pathway protein-1 is emerging as a promising marker for renal fibrosis [114, 115].

Pharmacogenomics integration

Proteins provide a dynamic reflection of cellular responses to drug treatments. To advance precision medicine, it is crucial to integrate genetic data with thorough proteomic analysis. The future of precision medicine depends on the union of pharmacogenomics and the innovative field of pharmacoproteomics, which utilizes proteomic tools for drug development [116]. Furthermore, integrating transcriptomics into this 'omics' approach is essential, considering the discrepancies that can exist between mRNA and protein expression levels [117]. Customized 'omics' strategies, incorporating both genetic and proteomic information, are helping to improve our understanding of disease mechanisms and drug responses. These integrated approaches are key to discovering, identifying, and monitoring new biomarkers across various complex conditions and their therapeutic interventions. By combining pharmacoproteomic profiles with pharmacogenomics databases, personalized treatment strategies may become a reality, enabling tailored therapies based on diagnostic results. It's evident that insights from diverse 'omics' disciplines—such as pharmacogenomics, transcriptomics, pharmacoproteomics, toxicoproteomics, and pharmacometabolomics—should not be considered independently, but rather as complementary components that provide a more holistic understanding [118].

Future directions in proteomics research

The field of understanding the body's responses to nutrition treatments has seen significant growth. The intersection of nutrigenetics, nutrigenomics, and the rise of 'omics' technologies is playing a major role in these developments [119]. The integration of various fields such as metabolomics, proteomics, and genetics, alongside anthropometric data and clinical biomarkers, will help us better understand the underlying mechanisms that regulate health [38]. Nutritional proteomics is rapidly advancing, with continuous breakthroughs happening in the field [120].

Recent advancements have shed light on the future of nutritional proteomics, particularly focusing on mass spectrometry and cutting-edge protein sequencing technologies that are expected to transform the landscape of proteomics [121]. Afzaal *et al.* [7] have explored the wide-ranging potential of proteomics in the areas of food authentication, quality control, and safety, demonstrating how proteomics can have applications across the food industry.

Looking ahead to 2035, it's projected that alternative proteins derived from plants, microorganisms, and animal cells could make up 11% of global protein consumption, with possibilities for that figure to increase to 22% with technological advancements and regulatory support. Such a shift, particularly towards plant-based options like meat and eggs, could have far-reaching environmental benefits. These include reducing carbon emissions to the level of Japan's annual output, saving enough water to meet London's needs for 40 years, and protecting biodiversity while improving food security. The alternative protein market, which is valued at $290 billion, is seen as a key component in creating a more sustainable food system, according to a report by Blue Horizon and the Boston Consulting Group.

Conclusion

In conclusion, nutritional proteomics has great potential for advancing our understanding of the complex relationship between diet, proteins, and overall health. Investigating nutrition at a molecular level allows us to uncover mechanisms involved in disease prevention, early detection, and tailored treatments. As technologies continue to evolve and integrate with other 'omics' disciplines, nutritional proteomics will offer new opportunities for personalized medicine. Ongoing research and collaborative efforts will be essential in realizing the full potential of this field, bringing personalized nutrition into mainstream healthcare practices.

Acknowledgments: I would like to sincerely thank the writers of the articles and resources cited in this review. Their work has been invaluable in shaping the development of this manuscript. Special thanks to the Department of Biochemistry at King Abdulaziz University, Kingdom of Saudi Arabia, for providing the support and time necessary to complete this project.

Conflict of Interest: None

Financial Support: None

Ethics Statement: None

References

1. Sveinsdóttir H, Martin SA, Vilhelmsson OT. Application of proteomics to fish processing and quality, 3rd ed.; In: Benjamin K, ed. Simpson, Publisher: Wiley-Blackwell, United States; 2012. p. 154-96. doi:10.1002/9781118308035.ch22
2. Tomanek L. Environmental proteomics: changes in the proteome of marine organisms in response to environmental stress, pollutants, infection, symbiosis, and development. Annu Rev Mar Sci. 2011;3:373-99. doi:10.1146/annurev-marine-120709-142729
3. Amiri-Dashatan N, Koushki M, Abbaszadeh HA, Rostami-Nejad M, Rezaei-Tavirani M. Proteomics applications in health: biomarker and drug discovery and food industry. Iran J Pharm Res. 2018;17(4):1523-36.
4. Schweigert FJ. Nutritional proteomics: methods and concepts for research in nutritional science. Ann Nutr Metab. 2007;51(2):99-107. doi:10.1159/000102101
5. Sellami M, Bragazzi NL. Nutrigenomics and breast cancer: state-of-art, future perspectives and insights for prevention. Nutrients. 2020;12(2):512. doi:10.3390/nu12020512
6. Carbonaro M. Proteomics: present and future in food quality evaluation. Trends Food Sci Technol. 2004;15(3-4):209-16. doi:10.1016/j.tifs.2003.09.020
7. Afzaal M, Saeed F, Hussain M, Shahid F, Siddeeg A, Al-Farga A. Proteomics as a promising biomarker in food authentication, quality and safety: a review. Food Sci Nutr. 2022;10(7):2333-46. doi:10.1002/fsn3.2842
8. Monti M, Cozzolino M, Cozzolino F, Tedesco R, Pucci P. Functional proteomics: protein-protein interactions in vivo. Ital J Biochem. 2007;56(4):310-4.
9. Banks RE, Dunn MJ, Hochstrasser DF, Sanchez JC, Blackstock W, Pappin DJ, et al. Proteomics: new perspectives, new biomedical opportunities. Lancet. 2000;356(9243):1749-56.
10. Serpa JJ, Parker CE, Petrotchenko EV, Han J, Pan J, Borchers CH. Mass spectrometry-based structural proteomics. Eur J Mass Spectrom. 2012;18(2):251-67. doi:10.1255/ejms.1178
11. Chemical proteome mining. Chair of Organic Chemistry II, Technische Universität München, n.d. [Accessed 27 Aug 2023]. Available from: https://www.bio.nat.tum.de/oc2/research/chemical-proteome-mining/
12. Schaeffer RD, Zhang J, Kinch LN, Pei J, Cong Q, Grishin NV. Classification of domains in predicted structures of the human proteome. Proc Natl Acad Sci U S A. 2023;120(12):e2214069120.
13. Wilson-Frank C. Proteomics in the evaluation of nutraceuticals and functional foods. In: Gupta R, Srivastava A, Lall R, eds. Nutraceuticals in Veterinary Medicine, 3rd ed.; Springer: Cham; 2019. pp. 52. doi:10.1007/978-3-030-04624-8_52
14. Karczewski KJ, Snyder MP. Integrative omics for health and disease. Nat Rev Genet. 2018;19(5):299-310. doi:10.1038/nrg.2018.4
15. Cifuentes A. Foodomics, foodome and modern food analysis. TrAC Trends Analyt Chem. 2017;96:1. doi:10.1016/j.trac.2017.09.001
16. Jagadeesh DS, Kannegundla U, Reddy RK. Application of proteomic tools in food quality and safety. Adv Anim Vet Sci. 2017;5(5):213-25.
17. Raposo de Magalhães CS, Cerqueira MA, Schrama D, Moreira MJ, Boonanuntanasarn S, Rodrigues PM. A proteomics and other omics approach in the context of farmed fish welfare and biomarker discovery. Rev Aquac. 2020;12(1):122-44. doi:10.1111/raq.12308
18. Creydt M, Fischer M. Food authentication in real life: How to link nontargeted approaches with routine analytics? Electrophoresis. 2020;41(20):1665-79. doi:10.1002/elps.202000030
19. Bolek S. Consumer knowledge, attitudes, and judgments about food safety: a consumer analysis. Trends Food Sci Technol. 2020;102:242-8. doi:10.1016/j.tifs.2020.03.009
20. Fuchs D, Winkelmann I, Johnson IT, Mariman E, Wenzel U, Daniel H. Proteomics in nutrition research: principles, technologies and applications. Br J Nutr. 2005;94(3):302-14.
21. Gallardo JM, Ortea I, Carrera M. Proteomics and its applications for food authentication and food-technology research. TrAC Trends Anal Chem. 2013;52:135-41. doi:10.1016/j.trac.2013.05.019

22. Zhan X, Li B, Zhan X, Schlüter H, Jungblut PR, Coorssen JR. Innovating the concept and practice of two-dimensional gel electrophoresis in the analysis of proteomes at the proteoform level. Proteomes. 2019;7(4):36. doi:10.3390/proteomes7040036
23. Cupp-Sutton KA, Wu S. High-throughput quantitative top-down proteomics. Mol Omics. 2020;16(2):91-9. doi:10.1039/c9mo00154a
24. Dupree EJ, Jayathirtha M, Yorkey H, Mihasan M, Petre BA, Darie CC. A critical review of bottom-up proteomics: the good, the bad, and the future of this field. Proteomes. 2020;8(3):14. doi:10.3390/proteomes8030014
25. Piersimoni L, Kastritis PL, Arlt C, Sinz A. Cross-linking mass spectrometry for investigating protein conformations and protein-protein interactions─ a method for all seasons. Chem Rev. 2021;122(8):7500-31. doi:10.1021/acs.chemrev.1c00786
26. Li D, Yi J, Han G, Qiao L. MALDI-TOF mass spectrometry in clinical analysis and research. ACS Meas Sci Au. 2022;2(5):385-404. doi:10.1021/acsmeasuresciau.2c00019
27. Birhanu AG. Mass spectrometry-based proteomics as an emerging tool in clinical laboratories. Clin Proteom. 2023;20(1):32. doi:10.1186/s12014-023-09424-x
28. Karpievitch YV, Polpitiya AD, Anderson GA, Smith RD, Dabney AR. Liquid chromatography mass spectrometry-based proteomics: biological and technological aspects. Ann Appl Stat. 2010;4(4):1797-823. doi:10.1214/10-AOAS341
29. Sangeetha J, Shettar AK, Thangadurai D, Dandin CJ, Hospet R, Sheth BP, et al. Whole protein analysis using LC-MS/MS for food authentication. InProteomics for food authentication 2020 May 7 (pp. 105-120). CRC Press.
30. Endalifer ML, Diress G. Epidemiology, predisposing factors, biomarkers, and prevention mechanism of obesity: a systematic review. J Obes. 2020;2020:1-8. doi:10.1155/2020/6134362
31. Chaudhary N, Kumar V, Sangwan P, Pant NC, Saxena A, Joshi S, et al. Personalized nutrition and-omics. Compr Foodomics. 2021:495-507. doi:10.1016/B978-0-08-100596-5.22880-1
32. Ikizler TA. Using and interpreting serum albumin and prealbumin as nutritional markers in patients on chronic dialysis. Semin Dial. 2014;27(6):590-2.
33. Marcason W. Should albumin and prealbumin be used as indicators for malnutrition? J Acad Nutr Diet. 2017;117(7):1144.
34. Peveler WJ, Yazdani M, Rotello VM. Selectivity and specificity: pros and cons in sensing. ACS Sens. 2016;1(11):1282-5.
35. Kussmann M, Panchaud A, Affolter M. Proteomics in nutrition: status quo and outlook for biomarkers and bioactives. J Proteome Res. 2010;9(10):4876-87.
36. Romagnolo DF, Milner JA. Opportunities and challenges for nutritional proteomics in cancer prevention. J Nutr. 2012;142(7):1360S-9S. doi:10.3945/jn.111.151803
37. Suhre K, McCarthy MI, Schwenk JM. Genetics meets proteomics: perspectives for large population-based studies. Nat Rev Genet. 2021;22(1):19-37. doi:10.1038/s41576-020-0268-2
38. Keijer J, Escoté X, Galmés S, Palou-March A, Serra F, Aldubayan MA, et al. Omics biomarkers and an approach for their practical implementation to delineate health status for personalized nutrition strategies. Crit Rev Food Sci Nutr. 2023:1-29. doi:10.1080/10408398.2023.2198605
39. Wang M, Hng TM. HbA1c: more than just a number. Aust J Gen Pract. 2021;50(9):628-32. Available from: https://search.informit.org/doi/10.3316/informit.046409063840494
40. Naryzny SN, Legina OK. Haptoglobin as a biomarker. Biochem Mosc Suppl B Biomed Chem. 2021;15(3):184-98. doi:10.1134/S1990750821030069
41. Shinozuka T, Kanda M, Kodera Y. Site-specific protein biomarkers in gastric cancer: a comprehensive review of novel biomarkers and clinical applications. Expert Rev Mol Diagn. 2023;23(8):701-12. doi:10.1080/14737159.2023.2232298
42. Köberle B, Schoch S. Platinum complexes in colorectal cancer and other solid tumors. Cancers (Basel). 2021;13(9):2073. doi:10.3390/cancers13092073
43. Kim SY, Lee JP, Shin WR, Oh IH, Ahn JY, Kim YH. Cardiac biomarkers and detection methods for myocardial infarction. Mol Cell Toxicol. 2022;18(4):443-55. doi:10.1007/s13273-022-00287-1

44. Smith SE, Muir J, Kalabalik-Hoganson J. Procalcitonin in special patient populations: guidance for antimicrobial therapy. Am J Health Syst Pharm. 2020;77(10):745-58. doi:10.1093/ajhp/zxaa089
45. Cazzato G, Colagrande A, Lospalluti L, Ingravallo G, Cascardi E, Dellino M, et al. Histological hallmarks of malignant melanoma. melanoma - standard of care, challenges, and updates in clinical research. IntechOpen; 2023. Italy. doi:10.5772/intechopen.106638
46. Dhara K, Mahapatra DR. Review on electrochemical sensing strategies for C-reactive protein and cardiac troponin I detection. Microchem J. 2020;156:104857. doi:10.1016/j.microc.2020.104857
47. Malmgren L, Öberg C, den Bakker E, Leion F, Siódmiak J, Åkesson A, et al. The complexity of kidney disease and diagnosing it - cystatin C, selective glomerular hypofiltration syndromes and proteome regulation. J Intern Med. 2023;293(3):293-308.
48. Yi TT, Yu JM, Liang YY, Wang SQ, Lin GC, Wu XD. Identification of cystic fibrosis transmembrane conductance regulator as a prognostic marker for juvenile myelomonocytic leukemia via the whole-genome bisulfite sequencing of monozygotic twins and data mining. Transl Pediatr. 2022;11(9):1521-33.
49. Balkanov SK, Trajkova S, Pivkova-Veljanovska A, Spasovski D, Ridova N, Kalcev G, et al. Chromosomal aberrations and bence-jones proteins as a significant biomarkers in multiple myeloma. Lett Appl Nano Bioscience. 2023;12(3):74. doi:10.33263/LIANBS123.074
50. Yan Y, Yeon SY, Qian C, You S, Yang W. On the road to accurate protein biomarkers in prostate cancer diagnosis and prognosis: current status and future advances. Int J Mol Sci. 2021;22(24):13537. doi:10.3390/ijms222413537
51. Ligorio F, Fucà G, Zattarin E, Lobefaro R, Zambelli L, Leporati R, et al. The pan-immune-inflammation-value predicts the survival of patients with human epidermal growth factor receptor 2 (HER2)-positive advanced breast cancer treated with first-line taxane-trastuzumab-pertuzumab. Cancers (Basel). 2021;13(8):1964. doi:10.3390/cancers13081964
52. Goryacheva OA, Ponomaryova TD, Drozd DD, Kokorina AA, Rusanova TY, Mishra PK, et al. Heart failure biomarkers BNP and NT-proBNP detection using optical labels. TrAC Trends Anal Chem. 2022;146:116477. doi:10.1016/j.trac.2021.116477
53. Khadir A, Tiss A. Proteomics approaches towards early detection and diagnosis of cancer. J Carcinog Mutagen. 2023;14:1-16.
54. Ősz Á, Lánczky A, Győrffy B. Survival analysis in breast cancer using proteomic data from four independent datasets. Sci Rep. 2021;11(1):16787. doi:10.1038/s41598-021-96340-5
55. Irimie AI, Braicu C, Pasca S, Magdo L, Gulei D, Cojocneanu R, et al. Role of key micronutrients from Nutrigenetic and nutrigenomic perspectives in cancer prevention. Medicina (Kaunas). 2019;55(6):283. doi:10.3390/medicina55060283
56. Irimie AI, Braicu C, Pileczki V, Petrushev B, Soritau O, Campian RS, et al. Knocking down of p53 triggers apoptosis and autophagy, concomitantly with inhibition of migration on SSC-4 oral squamous carcinoma cells. Mol Cell Biochem. 2016;419(1-2):75-82.
57. Schroll MM, Hummon AB. Employing proteomics to understand the effects of nutritional intervention in cancer treatment. Anal Bioanal Chem. 2018;410(25):6371-86. doi:10.1007/s00216-018-1219-z
58. Zhou Y, Lih TM, Pan J, Höti N, Dong M, Cao L, et al. Proteomic signatures of 16 major types of human cancer reveal universal and cancer-type-specific proteins for the identification of potential therapeutic targets. J Hematol Oncol. 2020;13(1):170. doi:10.1186/s13045-020-01013-x
59. Fortmann SP, Burda BU, Senger CA, Lin JS, Beil TL, O'Connor E, et al. Preventive services task force evidence syntheses, formerly systematic evidence reviews. In Vitamin, Mineral, and Multivitamin Supplements for the Primary Prevention of Cardiovascular Disease and Cancer: A Systematic Evidence Review for the U.S. Preventive Services Task Force; Agency for Healthcare Research and Quality (US): Rockville, MD, USA, 2013.
60. Juneja S, Rathore AS, Sharma K, Shetty D, Jain A. Antioxidant-oxidant index as a biomarker in oral potentially malignant disorders and oral squamous cell carcinoma: a biochemical study. J Clin Diagn Res. 2017;11(3):ZC05-8.
61. Esquivel-Chirino C, Bolaños-Carrillo MA, Carmona-Ruiz D, Lopéz-Macay A, Hernández-Sánchez F, Montés-Sánchez D, et al. The protective

role of cranberries and blueberries in oral cancer. Plants (Basel). 2023;12(12):2330. doi:10.3390/plants12122330

62. Galvão De Podestá OP, Peres SV, Salaroli LB, Cattafesta M, De Podestá JRV, von Zeidler SLV, et al. Consumption of minimally processed foods as protective factors in the genesis of squamous cell carcinoma of the head and neck in Brazil. PLoS One. 2019;14(7):e0220067. doi:10.1371/journal.pone.0220067
63. Weber DD, Aminzadeh-Gohari S, Tulipan J, Catalano L, Feichtinger RG, Kofler B. Ketogenic diet in the treatment of cancer - Where do we stand? Mol Metab. 2020;33:102-21. doi:10.1016/j.molmet.2019.06.026
64. Saraswat M, Mäkitie A, Agarwal R, Joenväärä S, Renkonen S. Oral squamous cell carcinoma patients can be differentiated from healthy individuals with label-free serum proteomics. Br J Cancer. 2017;117(3):376-84. doi:10.1038/bjc.2017.172
65. Azamjah N, Soltan-Zadeh Y, Zayeri F. Global trend of breast cancer mortality rate: a 25-year study. Asian Pac J Cancer Prev. 2019;20(7):2015-20. doi:10.31557/APJCP.2019.20.7.2015
66. Li KW, Ganz AB, Smit AB. Proteomics of neurodegenerative diseases: analysis of human post-mortem brain. J Neurochem. 2019;151(4):435-45. doi:10.1111/jnc.14603
67. Bissonauth V, Shatenstein B, Ghadirian P. Nutrition and breast cancer among sporadic cases and gene mutation carriers: an overview. Cancer Detect Prev. 2008;32(1):52-64.
68. Neagu AN, Jayathirtha M, Whitham D, Mutsengi P, Sullivan I, Petre BA, et al. Proteomics-based identification of dysregulated proteins in breast cancer. Proteomes. 2022;10(4):35. doi:10.3390/proteomes10040035
69. Mohanty V, Subbannayya Y, Patil S, Puttamallesh VN, Najar MA, Datta KK, et al. Molecular alterations in oral cancer using high-throughput proteomic analysis of formalin-fixed paraffin-embedded tissue. J Cell Commun Signal. 2021;15(3):447-59. doi:10.1007/s12079-021-00609-3
70. Daily A, Ravishankar P, Harms S, Klimberg VS. Using tears as a non-invasive source for early detection of breast cancer. PLoS One. 2022;17(4):e0267676. doi:10.1371/journal.pone.0267676
71. Marino P, Pepe G, Basilicata MG, Vestuto V, Marzocco S, Autore G, et al. Potential role of natural antioxidant products in oncological diseases. Antioxidants (Basel). 2023;12(3):704. doi:10.3390/antiox12030704
72. Dai H, Much AA, Maor E, Asher E, Younis A, Xu Y, et al. Global, regional, and national burden of ischaemic heart disease and its attributable risk factors, 1990-2017: results from the global burden of disease study 2017. Eur Heart J Qual Care Clin Outcomes. 2022;8(1):50-60. doi:10.1093/ehjqcco/qcaa076
73. Wong ND, Budoff MJ, Ferdinand K, Graham IM, Michos ED, Reddy T, et al. Atherosclerotic cardiovascular disease risk assessment: an American society for preventive cardiology clinical practice statement. Am J Prev Cardiol. 2022;10:100335. doi:10.1016/j.ajpc.2022.100335
74. Nurmohamed NS, Belo Pereira JP, Hoogeveen RM, Kroon J, Kraaijenhof JM, Waissi F, et al. Targeted proteomics improves cardiovascular risk prediction in secondary prevention. Eur Heart J. 2022;43(16):1569-77. doi:10.1093/eurheartj/ehac055
75. Hoogeveen RM, Pereira JPB, Nurmohamed NS, Zampoleri V, Bom MJ, Baragetti A, et al. Improved cardiovascular risk prediction using targeted plasma proteomics in primary prevention. Eur Heart J. 2020;41(41):3998-4007. doi:10.1093/eurheartj/ehaa648
76. Schumacher-Schuh A, Bieger A, Borelli WV, Portley MK, Awad PS, Bandres-Ciga S. Advances in proteomic and metabolomic profiling of neurodegenerative diseases. Front Neurol. 2022;12:792227. URL=https://www.frontiersin.org/articles/10.3389/fneur.2021.792227. doi:10.3389/fneur.2021.792227
77. Ho JE, Lyass A, Courchesne P, Chen G, Liu C, Yin X, et al. Protein biomarkers of cardiovascular disease and mortality in the community. J Am Heart Assoc. 2018;7(14):e008108. doi:10.1161/JAHA.117.008108
78. Andrews B, Murphy AE, Stofella M, Maslen S, Almeida-Souza L, Skehel JM, et al. Multidimensional dynamics of the proteome in the neurodegenerative and aging mammalian brain. Mol Cell Proteomics. 2022;21(2):100192. doi:10.1016/j.mcpro.2021.100192

79. Hosp F, Mann M. A primer on concepts and applications of proteomics in neuroscience. Neuron. 2017;96(3):558-71.
80. Poewe W, Seppi K, Tanner CM, Halliday GM, Brundin P, Volkmann J, et al. Parkinson disease. Nat Rev Dis Primers. 2017;3:17013.
81. Kaiser S, Zhang L, Mollenhauer B, Jacob J, Longerich S, Del-Aguila J, et al. A proteogenomic view of Parkinson's disease causality and heterogeneity. NPJ Parkinsons Dis. 2023;9(1):24. doi:10.1038/s41531-023-00461-9
82. Jain AP, Sathe G. Proteomics landscape of Alzheimer's disease. Proteomes. 2021;9(1):13. doi:10.3390/proteomes9010013
83. Hondius DC, van Nierop P, Li KW, Hoozemans JJ, van der Schors RC, van Haastert ES, et al. Profiling the human hippocampal proteome at all pathologic stages of Alzheimer's disease. Alzheimers Dement. 2016;12(6):654-68.
84. Hondius DC, Eigenhuis KN, Morrema THJ, van der Schors RC, van Nierop P, Bugiani M, et al. Proteomics analysis identifies new markers associated with capillary cerebral amyloid angiopathy in Alzheimer's disease. Acta Neuropathol Commun. 2018;6(1):46.
85. World Health Organization. World Health Statistics 2015. World Health Organization: Geneva, Switzerland; 2015.
86. Balashanmugam S. Proteomics in the treatment of infectious pathogens. J Proteomics Bioinform. 2022;15:604.
87. Zubair M, Wang J, Yu Y, Faisal M, Qi M, Shah AU, et al. Proteomics approaches: a review regarding an importance of proteome analyses in understanding the pathogens and diseases. Front Vet Sci. 2022;9:1079359. doi:10.3389/fvets.2022.1079359
88. Jean Beltran PM, Federspiel JD, Sheng X, Cristea IM. Proteomics and integrative omic approaches for understanding host–pathogen interactions and infectious diseases. Mol Syst Biol. 2017;13(3):922. doi:10.15252/msb.20167062
89. Sperk M, Van Domselaar R, Rodriguez JE, Mikaeloff F, Sá Vinhas B, Saccon E, et al. Utility of proteomics in emerging and re-emerging infectious diseases caused by RNA viruses. J Proteome Res. 2020;19(11):4259-74. doi:10.1021/acs.jproteome.0c00380
90. Greco TM, Cristea IM. Proteomics tracing the footsteps of infectious disease. Mol Cell Proteomics. 2017;16(4):S5-14.
91. Wang Z, Cryar A, Lemke O, Tober-Lau P, Ludwig D, Helbig ET, et al. A multiplex protein panel assay for severity prediction and outcome prognosis in patients with COVID-19: an observational multi-cohort study. EClinicalMedicine. 2022;49:101495. doi:10.1016/j.eclinm.2022.101495
92. Overmyer KA, Shishkova E, Miller IJ, Balnis J, Bernstein MN, Peters-Clarke TM, et al. Large-scale multi-omic analysis of COVID-19 severity. Cell Syst. 2021;12(1):23-40. doi:10.1016/j.cels.2020.10.003
93. Demichev V, Tober-Lau P, Lemke O, Nazarenko T, Thibeault C, Whitwell H, et al. A time-resolved proteomic and prognostic map of COVID-19. Cell Syst. 2021;12(8):780-94. doi:10.1016/j.cels.2021.05.005
94. Lee SE, Schulze KJ, Cole RN, Wu LS, Yager JD, Groopman J, et al. Biological systems of vitamin K: a plasma nutriproteomics study of subclinical vitamin K deficiency in 500 Nepalese children. OMICS. 2016;20(4):214-23.
95. Haoudi A, Bensmail H. Bioinformatics and data mining in proteomics. Expert Rev Proteomics. 2006;3(3):333-43. doi:10.1586/14789450.3.3.333
96. Sonsare PM, Gunavathi C. Investigation of machine learning techniques on proteomics: a comprehensive survey. Prog Biophys Mol Biol. 2019;149:54-69. doi:10.1016/j.pbiomolbio.2019.09.004
97. Su M, Zhang Z, Zhou L, Han C, Huang C, Nice EC. Proteomics, personalized medicine and cancer. Cancers (Basel). 2021;13(11):2512. doi:10.3390/cancers13112512
98. Louie AD, Huntington K, Carlsen L, Zhou L, El-Deiry WS. Integrating molecular biomarker inputs into development and use of clinical cancer therapeutics. Front Pharmacol. 2021;12:747194. doi:10.3389/fphar.2021.747194
99. Figarska SM, Rigdon J, Ganna A, Elmståhl S, Lind L, Gardner CD, et al. Proteomic profiles before and during weight loss: results from randomized trial of dietary intervention. Sci Rep. 2020;10(1):7913. doi:10.1038/s41598-020-64636-7
100. He QY, Chiu JF. Proteomics in biomarker discovery and drug development. J Cell Biochem. 2003;89(5):868-86.

101. Irvine GW, Nguyen S. An overview of the "-omics" fields at the forefront of next-generation personalized medicine and fundamental systems biology studies. Biomed Genet Genomics. 2019;4(2). doi:10.15761/BGG.1000147
102. Assadsangabi A, Evans CA, Corfe BM, Lobo A. Application of proteomics to inflammatory bowel disease research: current status and future perspectives. Gastroenterol Res Pract. 2019;2019:1426954. doi:10.1155/2019/142695
103. Bodaghi A, Fattahi N, Ramazani A. Biomarkers: promising and valuable tools towards diagnosis, prognosis and treatment of Covid-19 and other diseases. Heliyon. 2023;9(2):e13323. doi:10.1016/j.heliyon.2023.e13323
104. Vaz-Rodrigues R, Mazuecos L, Villar M, Urra JM, Gortázar C, de la Fuente J. Serum biomarkers for nutritional status as predictors in COVID-19 patients before and after vaccination. J Funct Foods. 2023;101:105412. doi:10.1016/j.jff.2023.105412
105. Farsi Y, Tahvildari A, Arbabi M, Vazife F, Sechi LA, Shahidi Bonjar AH, et al. Diagnostic, prognostic, and therapeutic roles of gut microbiota in COVID-19: a comprehensive systematic review. Front Cell Infect Microbiol. 2022;12:804644. doi:10.3389/fcimb.2022.804644
106. Rodriguez JAM, Bifano M, Roca Goma E, Plasencia CM, Torralba AO, Font MS, et al. Effect and tolerability of a nutritional supplement based on a synergistic combination of β-Glucans and selenium- and zinc-enriched Saccharomyces cerevisiae (ABB C1®) in volunteers receiving the influenza or the COVID-19 vaccine: a randomized, double-blind, placebo-controlled study. Nutrients. 2021;13(12):4347. doi:10.3390/nu13124347
107. Shama A, Soni T, Jawanda IK, Upadhyay G, Sharma A, Prabha V. The latest developments in using proteomic biomarkers from urine and serum for non-invasive disease diagnosis and prognosis. Biomark Insights. 2023;18:11772719231190218. doi:10.1177/11772719231190218
108. Fernández CA, Yan L, Louis G, Yang J, Kutok JL, Moses MA. The matrix metalloproteinase-9/neutrophil gelatinase-associated lipocalin complex plays a role in breast tumor growth and is present in the urine of breast cancer patients. Clin Cancer Res. 2005;11(15):5390-5.
109. Pories SE, Zurakowski D, Roy R, Lamb CC, Raza S, Exarhopoulos A, et al. Urinary metalloproteinases: noninvasive biomarkers for breast cancer risk assessment. Cancer Epidemiol Biomarkers Prev. 2008;17(5):1034-42. doi:10.1158/1055-9965.EPI-07-0365
110. Jedinak A, Curatolo A, Zurakowski D, Dillon S, Bhasin MK, Libermann TA, et al. Novel non-invasive biomarkers that distinguish between benign prostate hyperplasia and prostate cancer. BMC Cancer. 2015;15:259.
111. Watanabe Y, Hirao Y, Kasuga K, Tokutake T, Kitamura K, Niida S, et al. Urinary Apolipoprotein C3 is a potential biomarker for Alzheimer's disease. Dement Geriatr Cogn Dis Extra. 2020;10(3):94-104.
112. Pejcic M, Stojnev S, Stefanovic V. Urinary proteomics--A tool for biomarker discovery. Ren Fail. 2010;32(2):259-68.
113. Dihazi H, Müller GA, Lindner S, Meyer M, Asif AR, Oellerich M, et al. Characterization of diabetic nephropathy by urinary proteomic analysis: identification of a processed ubiquitin form as a differentially excreted protein in diabetic nephropathy patients. Clin Chem. 2007;53(9):1636-45.
114. Zhong X, Tu YJ, Li Y, Zhang P, Wang W, Chen SS, et al. Serum levels of WNT1-inducible signaling pathway protein-1 (WISP-1): a noninvasive biomarker of renal fibrosis in subjects with chronic kidney disease. Am J Transl Res. 2017;9(6):2920-32.
115. Wang B, Ding X, Ding C, Tesch G, Zheng J, Tian P, et al. WNT1-inducible-signaling pathway protein 1 regulates the development of kidney fibrosis through the TGF-β1 pathway. FASEB J. 2020;34(11):14507-20. doi:10.1096/fj.202000953R
116. Haider S, Pal R. Integrated analysis of transcriptomic and proteomic data. Curr Genomics. 2013;14(2):91-110. doi:10.2174/1389202911314020003
117. Ponomarenko EA, Krasnov GS, Kiseleva OI, Kryukova PA, Arzumanian VA, Dolgalev GV, et al. Workability of mRNA sequencing for predicting protein abundance. Genes (Basel). 2023;14(11):2065. doi:10.3390/genes14112065
118. Singh V. Current challenges and future implications of exploiting the omics data into nutrigenetics and nutrigenomics for personalized diagnosis and nutrition-based care. Nutrition. 2023;110:112002. doi:10.1016/j.nut.2023.112002

119. Pandita D, Pandita A. Omics technology for the promotion of nutraceuticals and functional foods. Front Physiol. 2022;13:817247. doi:10.3389/fphys.2022.817247
120. Shuken SR. An introduction to mass spectrometry-based proteomics. J Proteome Res. 2023;22(7):2151-71. doi:10.1021/acs.jproteome.2c00838
121. World Economic Forum. Alternative proteins will transform food, mitigate climate change and drive profits. Here's how. 2021. Available from: https://www.weforum.org/agenda/2021/03/alternative-proteins-will-transform-food-mitigate-climate-change-and-drive-profits.