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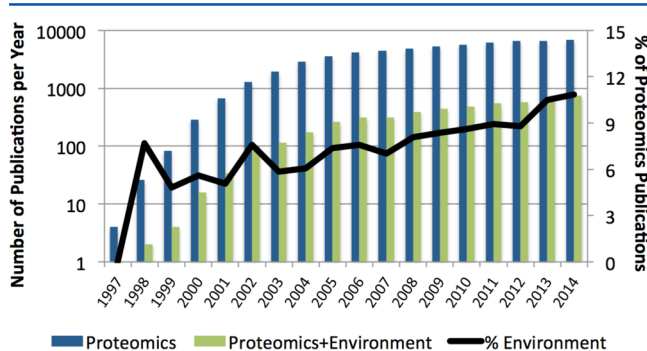
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## Recent Advances in Proteomics Applied to Elucidate the Role of Environmental Impacts on Human Health and Organismal Function

This Special Issue pays tribute to the importance of environmental factors as key determinants of the health of human populations and organismal functions supporting ecosystem services on planet Earth. Since the advent of the field of proteomics in 1997, the fraction of proteomic studies exploring the role of environmental factors has grown rapidly, now accounting for approximately 12% of all studies published annually, as revealed by data extracted from the PubMed database (Figure 1). While 12% is a substantial fraction, it still does not fully reflect the actual importance of environmental effects on human and ecological health.



**Figure 1.** PubMed database was searched using the term “proteomic\*” to capture all proteomics papers published between 1997 and 2014 (blue;  $n = 63\,339$ ). The term “environment\*” was then searched within this set of papers to determine the number of studies concerned with environmental proteomics (green;  $n = 5219$ ); the black line traces the fraction of total proteomics papers dealing with environmental factors.

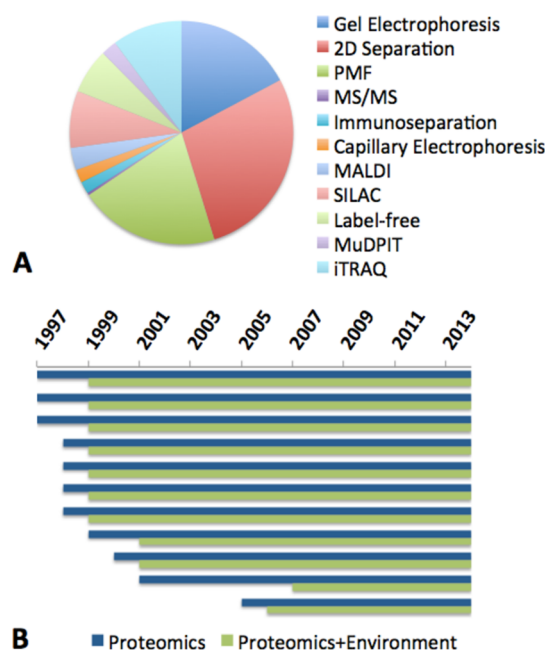
Recent studies show that environmental factors and lifestyle account for 90–95% of the risk of chronic diseases, including cancer, with hereditary traits contributing no more than 10%. Similarly,  $24 \pm 3\%$  of the global burden of disease and  $23 \pm 2\%$  of all deaths worldwide are attributable to environmental factors.<sup>2</sup>

To help address existing knowledge gaps concerning interactions between the environment and health, this Special Issue compiles 50 proteomic investigations. Three review papers take aim at important subjects, including mitochondrial targets for intervention in human disease,<sup>3</sup> the effects of motor vehicle exhaust on male reproductive function,<sup>4</sup> and the field of respiratory proteomics—from descriptive work to personalized medicine.<sup>5</sup> An additional study provides a toxicoproteomic perspective on the molecular basis of human health effects associated with exposure to anthropogenic polyfluorinated organic compounds.<sup>6</sup>

The vast landscape of cause-and-effect studies in environmental exposure science is organized here by target organism and experimental model, ranging from microorganisms<sup>7–14,52</sup> to murine<sup>15</sup> and human cell lines,<sup>16–21</sup> to plants,<sup>22,23</sup> to invertebrates,<sup>24,25,50</sup> and finally to mammals, including mice,<sup>26–31</sup> rats,<sup>32–34</sup> and humans.<sup>35–49,51</sup> Stressors investigated

include physical,<sup>17,30,31,50</sup> chemical,<sup>6,9,15,16,18,20,22,27,32</sup> and biological<sup>8,11,12,14,26,46</sup> agents as well as complex environmental changes such as diet,<sup>28,29,44</sup> air pollution,<sup>4</sup> and exposure to mixtures of metals.<sup>16</sup> Diseases addressed in this Special Issue include cancer,<sup>18,24,32,35,49,51</sup> celiac disease,<sup>41</sup> cystinuria,<sup>48</sup> diabetes,<sup>36,42,43</sup> endocrine disruption,<sup>25</sup> Legionnaires’ disease,<sup>21</sup> leishmaniasis,<sup>26</sup> leptospirosis,<sup>46</sup> liver disease,<sup>14,27</sup> microbial infections,<sup>11,14</sup> obesity,<sup>28</sup> painful bladder syndrome,<sup>45</sup> Parkinson’s disease,<sup>38</sup> preterm birth,<sup>37</sup> psoriasis,<sup>47</sup> psychotic disorders,<sup>33</sup> tuberculosis,<sup>10</sup> ulcerative colitis,<sup>39</sup> and studies on the role of the human microbiome.<sup>8,12,40</sup>

Research in environmental proteomics has a long history of quickly leveraging emergent tools from the general field of proteomics, a method migration process typically taking no more than 2 years on average (Figure 2). A search of the Web



**Figure 2.** Web of Science Core Collection database was searched for articles published between 1997 and 2014 in the field of environmental proteomics broken down by methodology employed; color-coded methodologies listed start at the top of the pie chart and are arranged in clockwise order (A). Further displayed is a timeline of the first citation in the literature for a technique used in the general field of proteomics (blue) and in environmental proteomics (green) (B). Proteomics research articles ( $n = 44\,291$ ) were determined by searching the above database with the publication type constrained to “articles” for “proteomic\*” in the topic field; environmental proteomics research articles ( $n = 2784$ ) were defined as the subset of proteomic articles that also used the term “environment\*”.

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of Science Core Collection for articles published between 1997 and 2014 shows common use of two-dimensional separation and gel electrophoresis for separation purposes; matrix-assisted laser desorption/ionization (MALDI) and tandem mass spectrometry for target identification; and stable isotope labeling with amino acids in cell culture (SILAC), label-free techniques, and isobaric tags for relative and absolute quantitation (iTRAQ) as preferred means of quantitative analysis.

Noteworthy methodologies and approaches highlighted in this Special Issue include the use of shotgun ecotoxicogenomic analyses,<sup>24</sup> ecotoxicoproteomics of human populations,<sup>6</sup> high-density programmable protein microarrays (NAPPA),<sup>49</sup> a new workflow for proteomic analysis of urinary exosomes,<sup>48</sup> metabolomic<sup>20,28,31,44,47</sup> and lipidomic analyses,<sup>31</sup> an enhanced metaproteomic approach for the study of the human microbiome,<sup>12</sup> and the use of interactome maps to characterize cellular response to viral infection.<sup>14</sup>

We hope you will enjoy reading the articles contained in this Special Issue, and we encourage you to consider environmental factors not only as a potential subject topic of your future work but also as a potent and omnipresent confounder that needs to be considered when interpreting results of proteomic and metabolomic research.

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### Notes

Views expressed in this editorial are those of the authors and not necessarily the views of the ACS.

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