

The Human Proteome Organization

A MISSION TO ADVANCE PROTEOME KNOWLEDGE*

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With the completion of the genome project, it has been viewed that the proteome is the next major challenge. With heightened expectations comes the need for organizing public effort. The Human Proteome Organization (HUPO)¹ was founded to regroup scientists in the public and private sectors engaged worldwide in various aspects of proteomics. Over the past year, HUPO has strived to develop a mission for itself and to begin the process of organizing its activities. The mission of HUPO as it is currently defined is to: 1) consolidate national and regional proteome organizations into a worldwide organization; 2) engage in scientific and educational activities to encourage the spread of proteomics technologies and disseminate knowledge pertaining to the human proteome and that of model organisms; and 3) assist in the coordination of public proteome initiatives. HUPO consists of three major geographic spheres that include Europe, Asia/Oceania, and the Americas. In addition to current national proteome organizations affiliated with HUPO, plans are underway to assist in the formation of additional national proteome organizations and to expand affiliations with HUPO of other organizations that have a significant proteomics component such as biochemistry and cell biology societies.

HUPO SCIENTIFIC ACTIVITIES AND INITIATIVES

A major aspect of the mission of HUPO is to promote initiatives in proteomics that benefit both the public and private sectors by providing open access to proteome-related data/information and knowledge for mining this functional compartment encoded by the genome. Illustrative of the mission of HUPO in this regard is a meeting that was convened by the organization in Leesburg, VA on October 7, 2001. In this meeting, we reviewed the state-of-the-art in proteomics, considered various opportunities and initiatives that may further our knowledge of the human proteome, and discussed the challenges that lie ahead.

Areas in need of development identified at the Leesburg meeting included development of proteomics resources and technologies, as well as development of protein informatics. It

was also considered beneficial to identify tissues and cell populations that could serve as model systems for cooperative proteomic studies involving multidisciplinary groups in different countries. Proteomics employ a combination of high tech approaches, in addition to old fashioned protein chemistry and biochemistry, and as a result there is a need and an opportunity to engage scientists in those countries that have not played a major role in genome initiatives. In addition to efforts in individual countries, proteome initiatives with a multi-national backing from governments, industry, and philanthropic organizations could contribute substantially to rallying and assembling the international community into an effective and powerful alliance to tackle the human proteome.

The recommendations resulting from the Leesburg meeting have led to a follow-up workshop that took place at the National Institutes of Health in Bethesda, MD on April 29, 2002. The workshop was attended by representatives from proteome organizations throughout the world and focused on five major topics as follows: 1) technological needs of expression proteomics; 2) informatics needs in proteomics; 3) identifying model cells and tissues for which there is broad interest; 4) the potential of developing a major initiative to characterize the plasma and serum proteomes; and 5) the prospect of a major initiative to make antibodies that recognize all of the proteins encoded by the genome. The presentations made by the chairs of the different planning committees, as well as the conclusions, are available on the HUPO web site (www.HUPO.org).

Although there has been skepticism regarding the prospects and the merits of a major proteome project, the initiatives envisioned by HUPO have clearly attracted substantial interest worldwide. For example, the need to have antibodies and ligands that recognize all of the proteins encoded for by the genome was articulated eloquently by Matthias Mann, the chair of the antibody planning committee. Researchers find themselves increasingly in need of specific antibodies against individual proteins, but no such resources are available publicly. The availability of a uniform set of antibodies, ligands, reagents, and standards would greatly benefit individual researchers and will enable proteome-scale investigations. A joint initiative to make antibodies that recognize all of the human proteins is illustrative of the type of initiatives that HUPO should catalyze as it will benefit investigators in both the private and public sectors.

From an informatics point of view, there is a substantial need for standardization in proteomics, including the adoption

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¹ The abbreviation used is: HUPO, Human Proteome Organization.

of data and annotation standards, a challenging issue that if not overcome will plague efforts at mining the proteome. A critical issue pertaining to proteome mining efforts has to do with organizing proteome-related data into a knowledge base. Thus, an initiative aimed at developing infrastructure resources and databases that regroup currently scattered proteome-related data and that would result in an annotated human proteome has substantial merits. Such an effort may well engage, in addition to informaticians, a community of investigators that is as diverse as needed to tackle the ensemble of human proteins. The constructed protein encyclopedia would be updated constantly with additional knowledge. A place to start could be the integration of proteomics initiatives targeted at specific cells, tissues, and organ sites being planned currently, such as a liver proteome project proposed by HUPO Asia/Oceania, with efforts in protein informatics, which would achieve the goals of data standardization on the one hand and data curation by the scientific community on the other.

HUPO SCIENTIFIC EXCHANGE AND EDUCATION AND TRAINING ACTIVITIES

In addition to activities aimed at developing resources and scientific initiatives in proteomics, there is a substantial need for dissemination of information and for organizing educational and training activities in proteomics. Annual gatherings to review the progress in the field, that attract not only established investigators but also post-doctoral and graduate students, are a must for any discipline, including proteomics. In addition to organizing regional meetings and workshops,

HUPO will host an Annual Congress that will serve as a major vehicle for sharing the latest data and technological innovations in the field. The meeting will provide a forum to discuss proteomic initiatives in individual countries and continents and will serve as a catalyst to foster collaborations between academia and the private sector. The first meeting, which is being planned for November 21–24, 2002 in Versailles, France, is expected to attract some 1500 participants worldwide. Further information about this year's Congress can be found at [www.hupo.org/new/First Annual HUPO Congress.html](http://www.hupo.org/new/First%20Annual%20HUPO%20Congress.html).

In addition to scientific meetings, HUPO will engage in a major educational and training effort in proteomics to help prepare the new generation of scientists in this emerging field. Plans to organize educational seminars, courses, and training workshops throughout the world are being sketched out currently. HUPO will also jointly sponsor similar activities with other public or private organizations.

Although the proteomics field holds much promise, the challenges ahead are formidable. There appears to be little substitute for an organized effort to move the field forward and effectively mine this most functional compartment encompassed by the proteome. HUPO intends to be a major contributor to this organized effort.

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