

11200 Rockville Pike Suite 302
Rockville, Maryland 20852
USA

American Society for Biochemistry and Molecular Biology, Office of Public Affairs

BENJAMIN W. CORB JULIE M. MCCLURE PH.D.
Director Science Fellow

eed for such an entity. This can be accomplished by providing long term fiscal support for creating
ning structure, actually capable of capturing only raw data but also various forms of processed
that would provide a central storehouse.

ING EXAMPLE: PROTEOMICS

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most significant hallmarks of biomedical research in this century, and perhaps one of the mos
d, has been the size and extent of data sets that have and continue to be generated by the new
es associated with genomic, transcriptomic, proteomic and metabolomic research (collectively the
iences or, by some definitions, systems biology). The microarray field that underpins
mics led the way but it has been supplanted by the massive outputs of next gen nucleic acid
g of vast numbers of human and other genomes. However, proteomic data, mostly generated by
hput mass spectrometry (MS), will eventually dwarf both of these and when coupled with
ic data that will likely be collected with similar technology, is destined to create an almost

looks for". This is particularly true for PTM analysis, as for most datasets a very limited number of PTMs are considered during data analysis. As a result, potential large amounts of information are not analyzed and the information contained therein lost if the raw data is not made available. This is enormously wasteful from both an intellectual and financial point of view. Finally, knowledge is a continuum and all data collected adds to it. This is particularly important to the bioinformaticians and other analyzers of processed and interpreted data, who can provide the larger p

