Integrative proteomics: prespective in complex system interpretation

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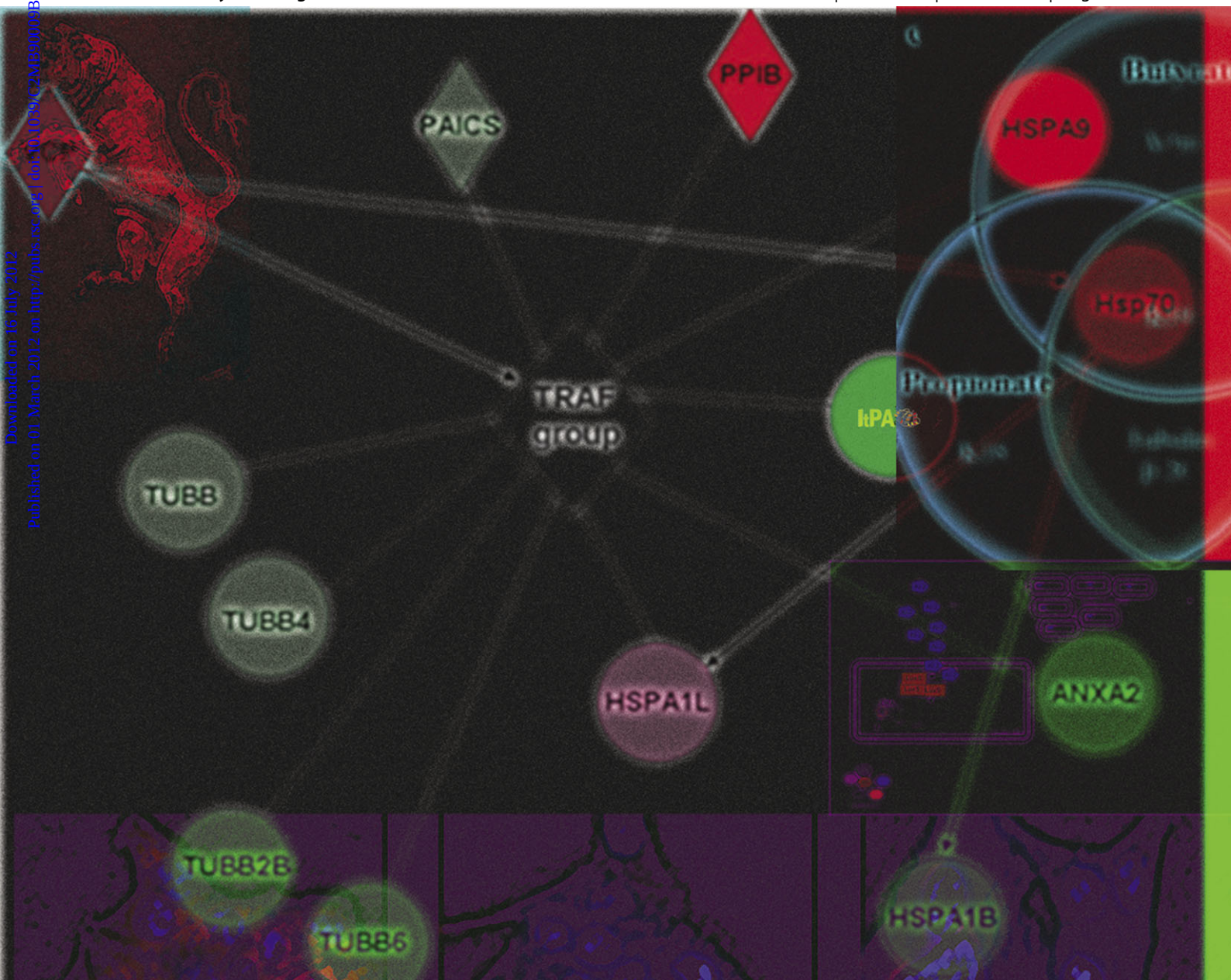

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EDITORIAL

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Directory Board of the Italian Proteomics Association (www.itpa.it) introduce this *Molecular BioSystems* themed issue on proteomics.

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EDITORIAL

Integrative proteomics: perspective in complex system interpretation

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In the development of new integrative molecular models of living organisms, proteomics investigations are becoming a key dataset. The hidden relationships between molecular effectors of specific biochemical phenomena are often explored by profiling the relative distribution of proteins levels, which may act as a molecular remnant of a defined mechanism. Proteome investigations often suffer from a limited in depth analysis of primary switch molecules such as the receptor tyrosine kinases whose proteomics investigations are deeply reviewed by Dr P. Huang (DOI: 10.1039/c1mb05327b). This is due to the bias we obtain in the evaluation of abundant proteins which may mask the direct analysis of low concentration regulatory polypeptides. This scenario is clearly observed when a network of ontological relationships is developed for the identified proteins in an open differential proteomics profile, where the experimentally mapped proteins in open proteomics profiling mostly lie on the periphery of such a relationship graph. The centre of the network is therefore computationally associated to molecular partners which have multiple interactions with the experimentally covered protein. This distribution is clearly visible in a number of papers in this themed issue on proteomics, following the Italian Proteomics Association's (www.itpa.it) National Congress in Turin (21st–24th June 2011).

The reported ontological network analyses have been clearly informative over the primary effector molecules. The paper from D. Pieragostino *et al.* (DOI: 10.1039/c1mb05357d) shows such a distribution following an investigation into the tears of patients with Primary open angle (POAG) and pseudoexfoliative glaucoma (PXG), which are the most common primary and secondary forms of glaucoma. The paper from F. Raimondo *et al.* (DOI: 10.1039/c2mb05390j) applies a functional protein network analysis to highlight the fundamental characteristics of renal cell carcinoma. Such an integrative evaluation, always on a clinical proteomics study, has been proposed by L. Giusti *et al.* (DOI: 10.1039/c2mb05394b) where the washing fluids of colon tract resection form patients with different stages of colon-rectal carcinoma have been investigated. Nevertheless, such complex data interpretation needs to be experimentally validated. The network analysis proposed by A. Sau *et al.* (DOI: 10.1039/c1mb05295k) provides key evidence on the potential mechanism of a new anti-cancer compound, NBDHEX, in treating osteosarcoma. The overall proteomics investigation coupled to functional network analysis provided key evidence for the identification of the TRAF2–GST P1 interaction mechanism in the action of this promising molecule. This paper experimentally demonstrates the results obtained from the ontological analysis. Such an experimental validation of a complex network analysis of nanoLC shotgun proteomics analysis has been successfully pursued in the paper from S. D'Aguanno *et al.* (DOI: 10.1039/c2mb05498a), where the involvement of nrf2 in response to curcumin in neuroblastoma cell models has been deduced by bioinformatic analysis and afterwards experimentally validated.

The bioinformatics repositories of functional relationships are biased toward human, mouse and rat data, due to the large campaigns of data collection which have been pursued in the last decade following biomedical research. Investigating other species is often complicated by the lack of appropriate bioinformatic tools and requires specific personal expertise. This is the case in the paper from C. Piras *et al.* (DOI: 10.1039/c1mb05385j) where the complex world of *E. Coli* sub-strains following phenotypic selection over multi-drug resistance biological pressure is investigated by state of the art proteomics tools. Therefore, following an integrative vision of biological systems investigation, it is also desirable to find correlations related to nucleic acid and metabolite profiles. The latter of which still requires the development of specific sensitive tools in order to tackle significant biological samples. In this light, the paper of A. D'Alessandro *et al.* (DOI: 10.1039/c1mb05358b) describes an important technological development for metabonomics investigation from blastocele fluids.

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In the end, we may consider the protein profile as a remnant of the molecular hallmarks of the biological and biochemical phenomena. As the Turin Shroud bears the image of Christ, the protein ontological network analysis bears the image of the key effectors of the biological system under investigation. Nevertheless, proteomics are always visible and open to direct experimental evaluation by scientists, unlike the Turin Shroud.

It is our hope that this series of themed issue papers will provide a new scenario towards integrative research in biochemistry, providing a novel framework for large international initiatives such as the Human Proteome Project.

