

protein expression and, most importantly, cross-analysis of common sample sets.

At present, only a small fraction of the complexity of the proteome is available to complement the genomic knowledge provided by ENCODE. Why are certain parts of the proteome expressed rarely if at all? C-HPP needs the insights of the regulatory environment of gene expression to contextualize the proteomic signal. Conversely, our view of the significance of changes in gene regulation is hindered by a lack of understanding of the consequences at the protein level. Thus, the integration of C-HPP and ENCODE outputs as well as metabolomic data will set the stage for defining the full complexity of phenomes in different biological states.

COMPETING FINANCIAL INTERESTS

The authors declare no competing financial interests.

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