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Intracellular localization gives first clue to protein function

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Jonathan B Weitzman
Email: jonathanweitzman@hotmail.com

Going from gene sequence to protein function presents a great challenge to genome biology. In the September 15 EMBO Reports, Simpson *et al*. suggest that the systematic identification of subcellular localization can significantly enhance our ability to assign functions to unknown ORFs (*EMBO Reports* 2000, **1**:287-292). Simpson et al. outline a strategy for such an approach. They adapted the Gateway cloning system to allow rapid, directional cloning of ORFs by recombination, and generate amino- and carboxy- terminal GFP (green fluorescence protein) fusions. The authors used protein localization in living cells to follow the GFP-tagged proteins and to categorize clones for further study. More than 80% of proteins localized to recognized structures such as the cytosol (18%), nucleus (12%), secretory pathway (28%), mitochondria (5%) or the cytoskeleton (3%). Combining compartmentalization data with bioinformatic analysis of the cDNA sequences offers a promising strategy for predicting protein function. The authors stress that this approach has features amenable to scale-up for high-throughput analysis - it is rapid, efficient and has potential for automation.

References

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