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Improved purification for proteomics

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Jonathan B Weitzman
Email: jonathanweitzman@hotmail.com

The TAP-tag (tandem affinity purification) methodology has been effectively used for genome-wide proteomic analysis in yeast. Applications in higher eukaryotes have been hindered by the technical difficulties resulting from expression of endogenous untagged proteins. In an Advanced Online Publication in Nature Biotechnology Daniel Forler and colleagues at the European Molecular Biology Laboratory in Germany, describe the 'iTAP strategy' that incorporates double-stranded RNAi technology to suppress endogenous protein expression (*Nature Biotechnology,* 16 December 2002, DOI:10.1038/nbt773). This approach was validated by isolating components of the exosome, a multienzyme complex of exoribonucleases, from *Drosophila* Schneider S2 cells using a tagged human Rrp4 protein. The iTAP strategy improved the yield and specificity of purification of *Drosophila* exosome components. Improved purification was also demonstrated for the heterodimeric nuclear export receptor NXF1-p15 and the Mago nashi protein complex. The iTAP approach is thus likely to facilitate functional proteomic projects in higher eukaryotes.

References

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