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Proteome purification

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In the March 5 Proceedings of the National Academy of Sciences, Braun *et al.* describe a methodology to perform high-throughput purification of human proteins using several affinity-tags (Proc Natl Acad Sci USA2002,99:2654-2659). They exploited the Gateway recombinational cloning system that employs a versatile 'master' vector for easy transfer into different expression vectors. They chose a test set of 32 human genes and expressed them in four different vectors with different affinity tagsL: the His6tag, calmodulin-binding peptide, glutathione-*S*-transferase or maltose-binding protein. Using different denaturing and nondenaturing purification conditions they were able to isolate around 80% of expressed proteins. Braun *et al.*demonstrated that the system can be easily scaled-up, and then applied the same approach to a set of 336 human cDNAs with a success rate of around 60%. This approach allows for optimization of protein purification on a proteome-scale.

References

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2. Global efforts in structural genomics.

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