In large-scale proteomics studies there is a temptation, after months of experimental work, to plug resulting data into a convenient—if poorly implemented—set of tools, which may neither do the data justice nor help answer the scientific question. In this paper we have captured key concerns, including arguments for community-wide open source software development and “big data” compatible solutions for the future. For the meantime, we have laid out ten top tips for data processing. With these at hand, a first large-scale proteomics analysis hopefully becomes less daunting to navigate. However there is clearly a real need for robust tools, standard operating procedures and general acceptance of best practises. Thus we submit to the proteomics community a call for a community-wide open set of proteomics analysis challenges—PROTEINCHALLENGE—that directly target and compare data analysis workflows, with the aim of setting a community-driven gold standard for data handling, reporting and sharing. This article is part of a Special Issue entitled: New Horizons and Applications for Proteomics [EuPA 2012].