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On the cover: A 2D LC-MS/MS-based proteomics approach has allowed identification of 1458 proteins in *Brassica napus* (canola) guard cells (*left*, two cells forming a stomate) and mesophyll cells (*right*, a mesophyll cell protoplast). The iTRAQ reporter ions in a peptide MS/MS spectrum indicate that the peptide containing protein is more abundant in guard cells (114 and 115) than in mesophyll cells (116 and 117). For details, see the article by Zhu *et al.*, pages 752–766.

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