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On the cover: Proline-rich sequence recognition driving protein assembly. The interaction profiles of the bifunctional CD2BP2-GYF and Tsg101-UEV adaptor domains were determined by selective epitope inhibition and SILAC-MS. The impact of the proline binding site for protein complex formation is reflected by high $^{13}\text{C}/^{12}\text{C}$ ratios of peptides from specific binding partners (highlighted in green). For details, see the articles by Kofler *et al.*, pages 2461–2473 and Schlundt *et al.*, pages 2474–2486.

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