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On the cover, an approach for a quantitative comparison of the MHC ligandome and the transcriptome is shown. From pairs of tumor and autologous normal tissues, both MHC ligands and mRNA were isolated and quantified. Using the differential N-terminal isotope coding (*dNIC*) strategy for modification of MHC bound peptides, several hundred peptide ratios and sequences were identified. RNA levels were assessed by gene chip analysis and correlated with their respective peptide presentation ratios. For details, see the article by Weinzierl *et al.*, pages 102–113.

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