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Erratum

Serum protein profiling by SELDI mass spectrometry: detection of multiple variants of serum amyloid alpha in renal cancer patients

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Correction to: Laboratory Investigation (2004) **84**, 845–856. doi:10.1038/labinvest.3700097

Due to a publisher error, two figures were displayed incorrectly. The correct figures are shown below:

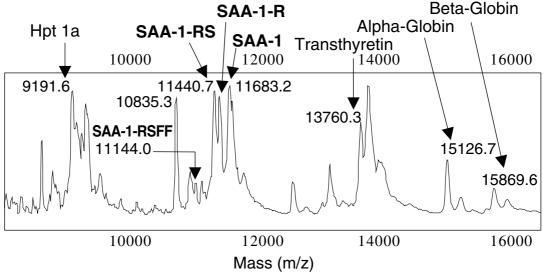


Figure 2 SELDI profile of patient R9 serum, using a laser intensity of 250. Proteins identified by in-gel tryptic digestion and peptide mapping are labelled and fit accurately to the expected average masses as given in Table 1. The RCC-related protein at $m/z = 10\,835.3\,\mathrm{Da}$ remains unidentified. The peak corresponding to SAA-1 des-R occurs at $m/z = 11\,526.5$.



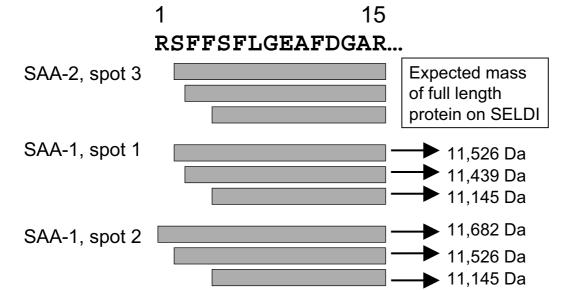


Figure 5 N-terminal sequences of SAA-1 and SAA-2 from 2-D electrophoresis as determined by in-gel tryptic digestion and measurement by MALDI Re-TOF mass spectrometry. All fragments terminated at arginine 15, the expected tryptic cleavage site. Of note are the two peptides spanning positions 3-15 (spots 1 and 3) and 5-15 (spots 1, 2 and 3), which correspond to uncommon N-terminal post-translationally modified variants of SAA-1 visualized simultaneously by SELDI (Figure 3). Expected masses are given of the full-length protein variant.