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CORRECTION

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Correction: Predictive chromatography of peptides and proteins as a complementary tool for proteomics

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Correction for 'Predictive chromatography of peptides and proteins as a complementary tool for proteomics' by Irina A. Tarasova *et al.*, *Analyst*, 2016, **141**, 4816–4832.

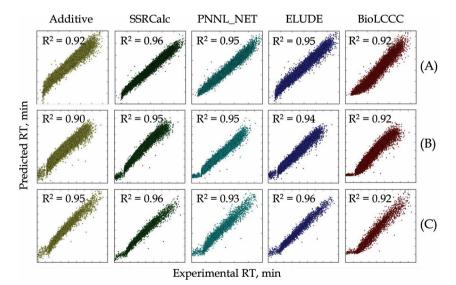
Within the Performance comparison section, on p. 4823, the text

"For example, the SSRCalc model demonstrated accuracies of 0.95 to $0.96R^2$ for data sets consisting of $\sim 12\,000$ HeLa tryptic peptides and ~ 3200 HeLa elastase peptides, but a lower correlation of $0.93R^2$ for ~ 9900 tryptic peptides identified in baker's yeast from ABRF 2015 iPRG study. PNNL NET's best result of $0.95R^2$ was obtained for the same 12 000 HeLa tryptic peptides, while its accuracy did not exceed $0.93R^2$ for the remaining data."

should be replaced with the following:

"The SSRCalc model demonstrated persistent accuracies of 0.95 to $0.96R^2$ for all considered data sets. PNNL NET's best result of $0.95R^2$ was obtained for the 12 000 HeLa tryptic peptides and the 9900 yeast tryptic peptides identified in baker's yeast from ABRF 2015 iPRG study, while its accuracy did not exceed $0.93R^2$ for the remaining data."

Also, Fig. 1 should be amended and the corrected version is shown here:



The Royal Society of Chemistry apologises for these errors and any consequent inconvenience to authors and readers.

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