



Cite this: *Analyst*, 2017, **142**, 2054

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

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DOI: 10.1039/c7an90034a

rsc.li/analyst

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.

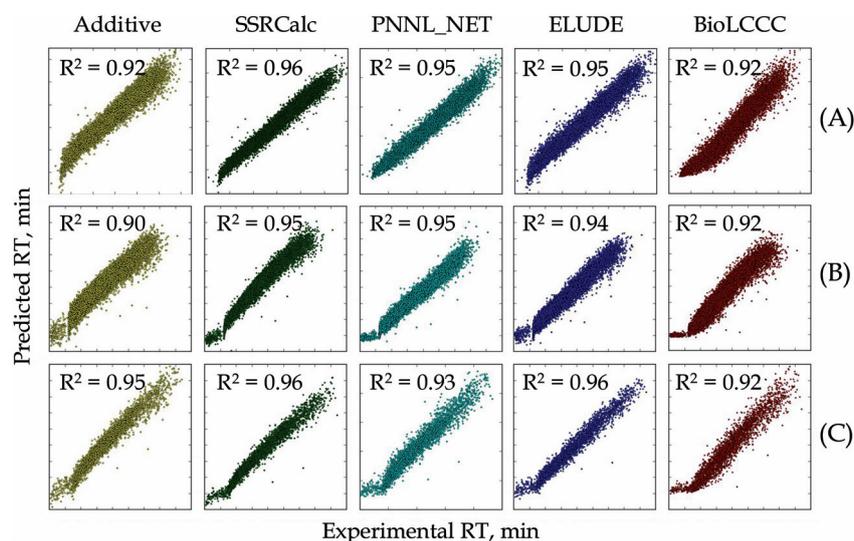
Within the **Performance comparison** section, on p. 4823, the text

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

should be replaced with the following:

“The SSRCalc model demonstrated persistent accuracies of 0.95 to 0.96 R^2 for all considered data sets. PNNL NET's best result of 0.95 R^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 0.93 R^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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