CORRECTION

Check for updates

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

Irina A. Tarasova,[a] Christophe D. Masselon,[b,c] Alexander V. Gorshkov[d] and Mikhail V. Gorshkov*[a,e]

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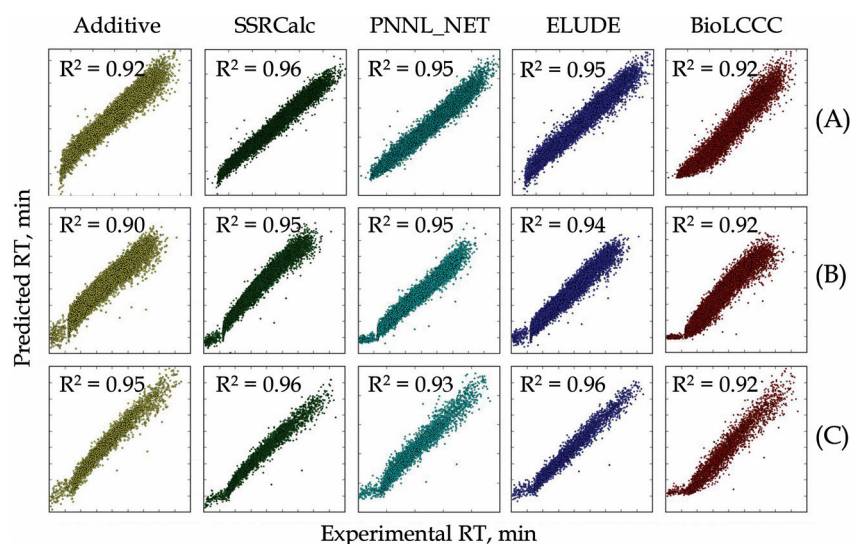
The Royal Society of Chemistry apologises for these errors and any consequent inconvenience to authors and readers.

[a]*Institute for Energy Problems of Chemical Physics, Russian Academy of Sciences, Moscow 119334, Russia. E-mail: mike.gorshkov@gmail.com*

[b]*CEA, iRTSV-BGE, Laboratoire d'Etude de la Dynamique des Protéomes, Grenoble, F-38000, France*

[c]*INSERM, U1038-BGE, F-38000 Grenoble, France*

[d]*N.N. Semenov Institute of Chemical Physics, Russian Academy of Sciences, Moscow 119991, Russia*

[e]*Moscow Institute of Physics and Technology (State University), Dolgoprudny, Moscow region 141700, Russia*