

Supplement to
Peptide retention time prediction yields improved
tandem mass spectrum identification for diverse
chromatography conditions

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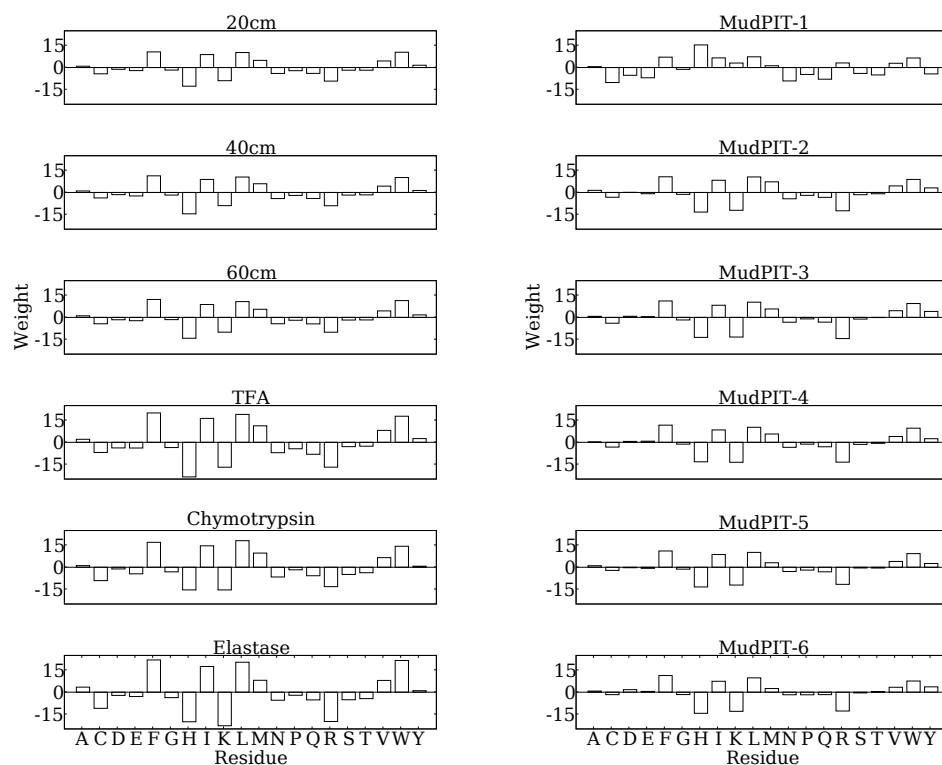


Figure 1: **Contributions to retention time (RT).** Shown are the support vector regression weights for the linear kernel for the 20 features corresponding to peptide amino acid composition; higher values indicate a positive contribution to RT.

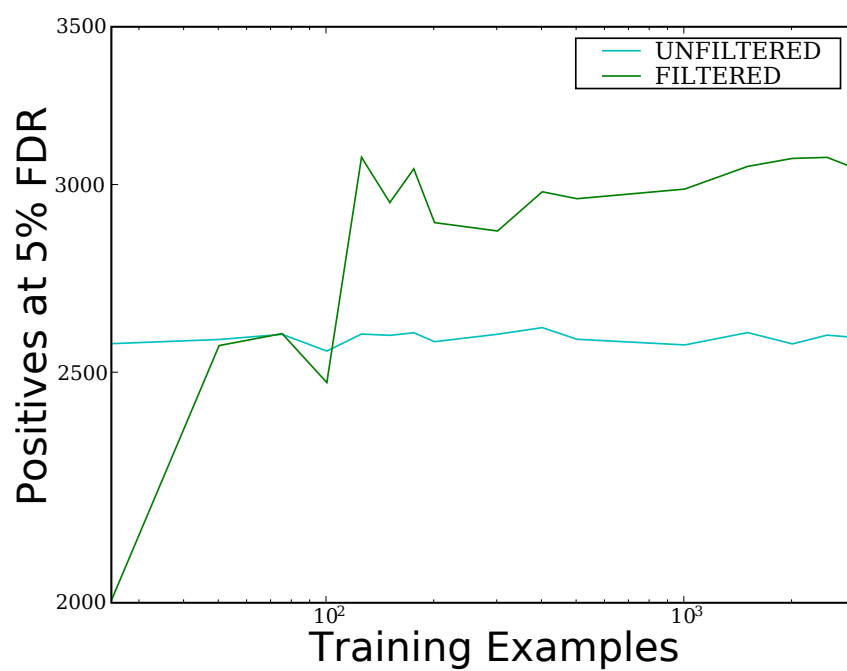


Figure 2: **Filtering performance as a function of number of training examples.** Shown are the number of true positives at 5% FDR vs the number of peptides used to train the retention time support vector regressor for the TFA data set.