

October 14, 2021

Dear Editor:

The enclosed manuscript, “Prosit Transformer: A transformer for prediction of MS2 spectrum intensities”, discusses the benefit of a promising deep learning technique, Transformers, for Mass Spectrometry-based Proteomics. We demonstrate a successful employment of the technology by retraining the Prosit model for predicting MS2 spectrum intensities. We call this new predictor Prosit Transformer, to distinguish it from its predecessors. We believe that this predictor is just a first of many Transformer-based predictors that will transform the future of analysis of data from mass spectrometers.

The manuscript is an original contribution and none of the work it describes has been published elsewhere, but we would like to keep the right to make it available through bioRxiv if needed. The manuscript will remain with you and will not be submitted elsewhere until you made a decision as to its suitability for publication in Journal of Proteome Research.

We suggest the following six experts in the analysis of proteomics data as potential reviewers:

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Sincerely,

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