

## Supplementary Material

### S1 Supplementary Tables

Table S1: Table showing the performance of Droppler in a 5-folds stratified cross-validation. The proteins involved in each train and test split shared less than 20% sequence identity. See Methods for an explanation of the performance metrics.

	Sen	Spe	BAC	Pre	MCC	AUC	AUPRC
Droppler	75	49	62	69	24	64	70

## S2 Supplementary Figures

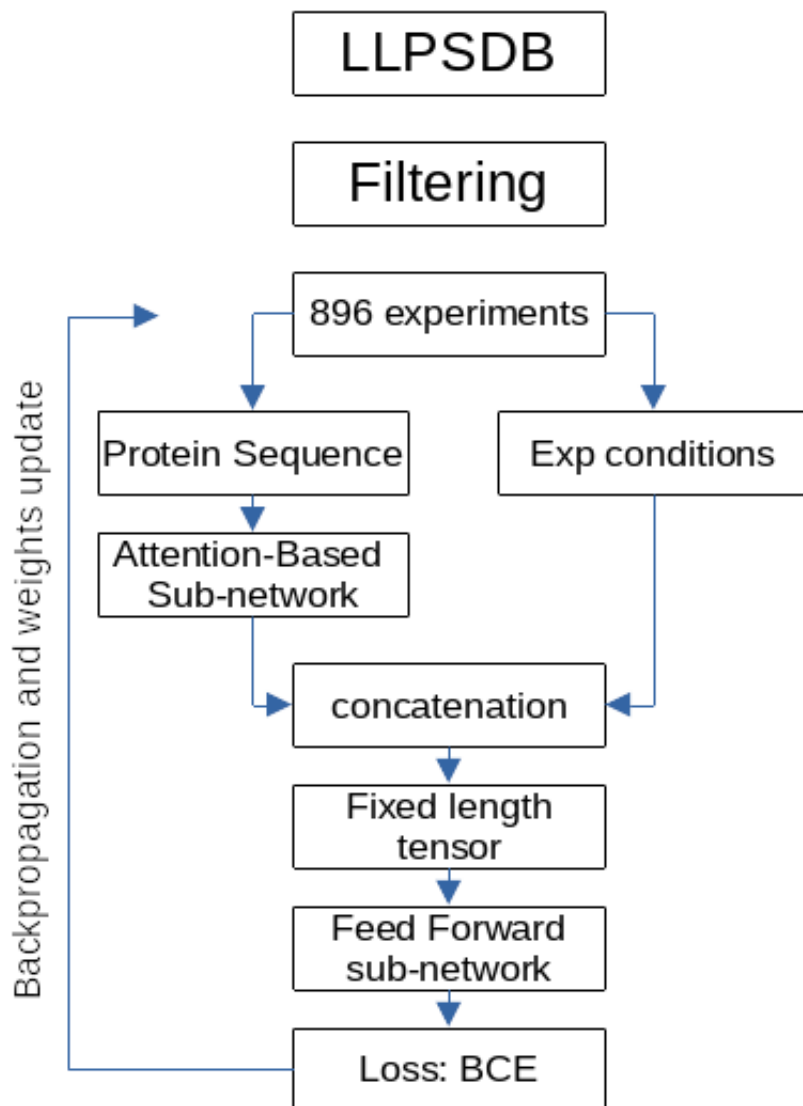


Figure S1: Diagram showing the pipeline of Droppler. From LLPSDB we extract all the annotated experiments. We filter them in order to remove experiments with missing data or inconsistent measure units and we end up with 896 experiments. Each experiment has a protein sequence and a set of experimental condition (protein concentration, salt concentration, PH, presence or absence of crowding factors and temperature). The neural network has two sub-networks: the first deals with the protein sequence (with a multi-head attention architecture) while the second one deals with the experimental conditions. The results of these two sub-networks is concatenated, resulting in a single, fixed length tensor. This tensor can be used to feed a feed forward module that provide the final output. The predicted outputs are compared with the ground truth using a binary cross entropy loss and back propagation is performed. The whole procedure is performed in an end-to-end fashion.

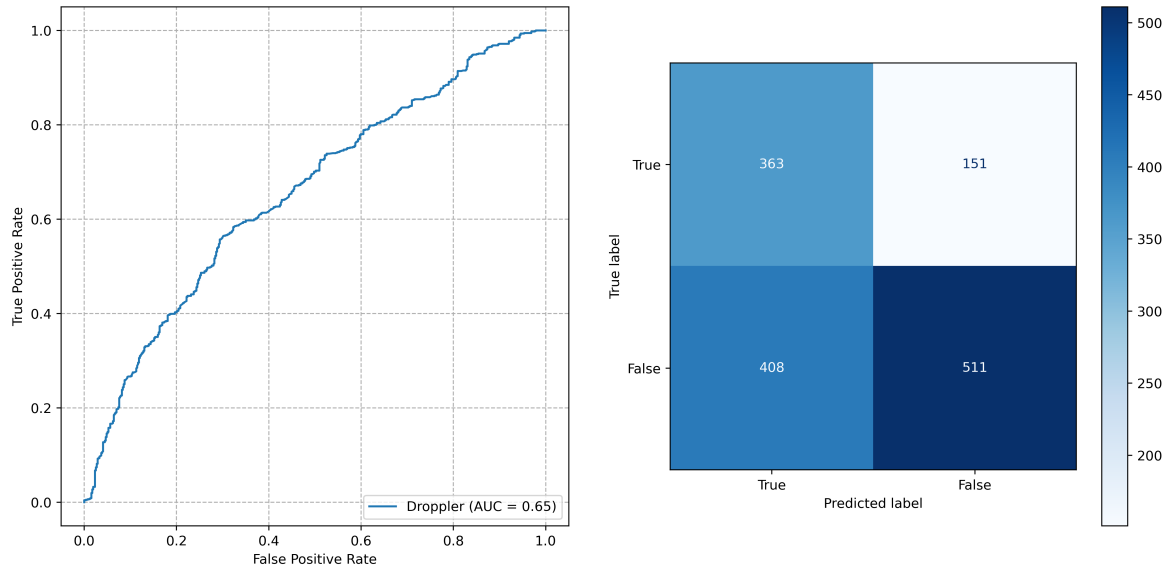


Figure S2: Figure showing the ROC curve (left plot) and the confusion matrix (right plot). These results have been obtained with the 5-folds cross-validation described in the paper.