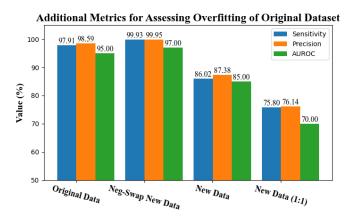
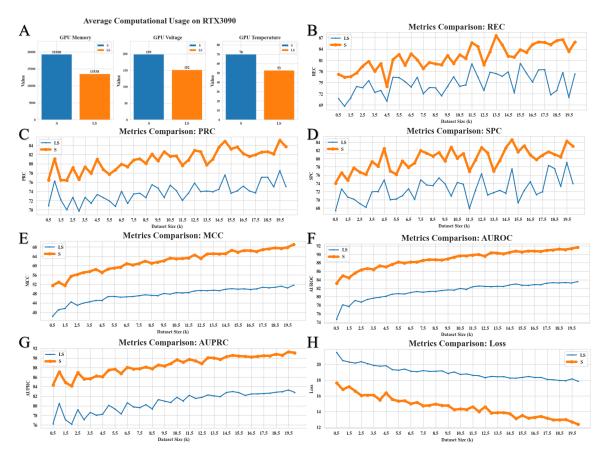
## Enhancing Cross-Domain Protein and Peptide Interaction with Re-trained Deep Learning Models —— Xin Cao et al.

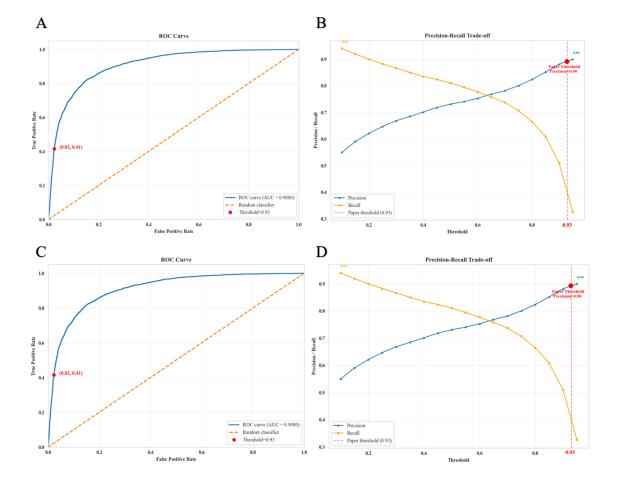
## **Supplementary Figures**



**Supplementary Fig. 1.** The Sensitivity, Precision and AUROC metrics of models trained on PPI-GNN's original dataset, original dataset with negative samples swapped with our new dataset, our new dataset, and our new dataset with positive samples: negative samples = 1:1.



Supplementary Fig. 2. Additional Metrics for Evaluating Short Protein Dataset Performance.



**Supplementary Fig. 3. (A-B)** ROC and Precision-Recall Analysis on Human-trained, Human-tested metrics. Red points indicate the metrics calculated when Threshold of Positive/Negative = 0.93. **(C-D)** ROC and Precision-Recall Analysis on Human-trained, Yeast-tested metrics. Red points indicate the metrics calculated when Threshold of Positive/Negative = 0.93.